



SEQUENCE LISTING

<110> Genetech, Inc.  
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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr  
35 40 45  
Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr  
50 55 60  
Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu  
65 70 75 80  
Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala  
85 90 95  
Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr  
100 105 110  
Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
115 120 125  
Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser  
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Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
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Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
180 185 190  
His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
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 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255  
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
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 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
35 40 45  
  
Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
50 55 60  
  
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile  
65 70 75 80  
  
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln  
85 90 95  
  
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly  
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Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro  
115 120 125  
  
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln  
130 135 140  
  
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu  
145 150 155 160  
  
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr  
165 170 175

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys  
180 185 190

Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His  
195 200 205

Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys  
210 215 220

Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn  
225 230 235 240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys  
245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln  
260 265 270

Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys  
275 280 285

Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu  
290 295 300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys  
305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Glu Gly Trp His Gly Arg His  
325 330 335

Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala  
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 8  
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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22

<210> 10  
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<212> DNA

<213> Homo sapiens

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<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu

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Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr		
65	70	75
80		
Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro		
85	90	95
Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr		
100	105	110
Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln		
115	120	125
Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln		
130	135	140
Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly		
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His Asp Pro Gly		

<210> 13  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 14  
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<210> 15  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 16  
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oligonucleotide probe

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ccgtgggtgc cccgcaccc agcaggggac aggcaactcg gaggggccag taaaggctga 780  
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agagatgggg cctggaggcc tggaggaagg ggccaggcc cacattcgt gggctccctg 900  
aatggcagcc tgagcacagc gttagccctt aataaacacc tgttggataa gccaaaaaaaa 960

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

Met Thr His Arg Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
180 185

<210> 19

<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 19  
tgctgtgcta ctccctgcaaa gcccc 24

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20  
tgcacacaaggc ggtgtcacag cacc 24

<210> 21  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21  
agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg 44

<210> 22  
<211> 1200  
<212> DNA  
<213> Homo sapiens

<400> 22  
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gaccgaccag ctgagcaggc ggcagatccg cgagttaccaa ctctacagca ggaccagtgg 180  
caagcacgtg caggtcacccg ggcgtcgcat ctccgcccacc gcccaggac gcaacaagtt 240  
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<210> 23  
<211> 205  
<212> PRT  
<213> Homo sapiens

<400> 23  
Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
1 5 10 15  
Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
20 25 30  
Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
35 40 45  
Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
50 55 60  
Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
65 70 75 80  
Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
85 90 95  
Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
100 105 110  
Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
115 120 125  
Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
130 135 140  
Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
145 150 155 160  
Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
165 170 175  
His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
180 185 190  
Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
195 200 205  
<210> 24  
<211> 28  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 24  
cagtagtga gggaccaggg cgccatga 28

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 25  
ccggtgacct gcacgtgctt gcc 24

<210> 26  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<220>  
<221> modified\_base  
<222> (21)..(21)  
<223> a, t, c or g

<400> 26  
gcggatctgc cgcctgctca nctggtcggt catggcgccc t 41

<210> 27  
<211> 2479  
<212> DNA  
<213> Homo sapiens

<400> 27  
actgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60  
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ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccc 180  
tccagtcatt ttgattttgc tggttatttt tttttcttt ttcttttcc caccacattg 240  
tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300  
ctttttctt gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
tcctggctg cccttagtgtg tgccgctgctg acaggaactt tgcactgt aatgagcgaa 420  
gcttgacctc agtgcctctt gggatcccgg agggcgtaac cgtactctac ctccacaaca 480  
accaaattaa taatgcttga ttccctgcag aactgcacaa tgcactgtcgt gtgcacacgg 540  
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tgaagcttga agagctgcac ctggatgaca actccatatac cacagtgggg gtggaaagacg 720  
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ccccaaatgc agcttctccg accactcagc ctcccccaccc ctctattcca aacccttagca 1440  
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gcagagaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560  
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catgggtgaa aatggccac agtttagtag gggcatcg tcaaggagc atagtcagcg 1680  
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ccacccatgc ctccatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860  
cgccccacag catggctcc cccttctgc tggcggcgt gatgggggc gcggatgat 1920  
tttgctggt ggtctgctc agcgtcttt gctggcatat gcacaaaaag gggcgctaca 1980  
cctcccgaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040  
ccaagaagga caactccatc ctggagatga cagaaaccag tttcagatc gtctcctaa 2100  
ataacgatca actccttaaa ggagattca gactgcagcc catttacacc ccaaatgggg 2160  
gcattaatta cacagactgc catatcccc acaacatgcg atactgcaac agcagcgtgc 2220  
cagacctgga gcactccat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280  
tagactctt agaacacact cgtgtgtgca cataaagaca cgcagattac atttgataaa 2340  
tgttacacag atgcatttgc gcatttgaat actctgtaat ttatacgggt tactatataa 2400  
tggatttaa aaaaagtgtct atctttcta tttcaagtttta attacaaaca gttttgttaac 2460  
tcttgcttt taaaatctt 2479

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu  
1 5 10 15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys  
20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser

130 135 140  
Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
145 150 155 160  
Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
165 170 175  
Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
180 185 190  
Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
195 200 205  
Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
210 215 220  
Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
225 230 235 240  
Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
245 250 255  
Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
260 265 270  
Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
275 280 285  
Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
290 295 300  
Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
305 310 315 320  
Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
325 330 335  
Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
340 345 350  
Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
355 360 365  
Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
370 375 380  
Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
385 390 395 400  
Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg  
405 410 415  
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val  
420 425 430  
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met

435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
660		

<210> 29  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 29  
 cggcttaccc ttatggcaac c

<210> 30

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30  
gcaggacaac cagataaaacc ac 22

<210> 31  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31  
acgcagattt gagaaggctg tc 22

<210> 32  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32  
ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac 46

<210> 33  
<211> 3449  
<212> DNA  
<213> Homo sapiens

<400> 33  
acttggagca agcggcggcg gcggagacag aggcagagggc agaagctggg gctccgtcct 60  
cgcctccac gagcgatccc cgaggagagc cgccggccctc ggcgaggcg a gaggccgac 120  
gaggaagacc cgggtggctg cgccccctgcc tcgccttcca ggcgcggcg gctgcagcct 180  
tgcccctctt gtcgccttgc aaaaatggaaa agatgcgtc aggctgcattt ctgctgatcc 240  
tcggacagat cgtcctcctc cctgccgagg ccagggagcg gtcacgtggg aggtccatct 300  
ctaggggcag acacgctcgg acccacccgc agacggccct tctggagagt tcctgtgaga 360  
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atgcaaaggt caaggagttc atcgtggaca tcttgcattt ctggacatt ggtcctgtatg 480  
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gcatcaacat ccctggctca tacgtctgca ggtgcaaaca aggctacatt ctcaactcgg 1020  
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<210> 34  
 <211> 915  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His  
225 230 235 240

Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile  
245 250 255

Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser  
260 265 270

Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His  
275 280 285

Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln  
290 295 300

Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala  
305 310 315 320

Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val  
325 330 335

Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu  
340 345 350

Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn  
355 360 365

Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr  
370 375 380

Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys  
385 390 395 400

Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu  
405 410 415

Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe  
420 425 430

Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu  
435 440 445

Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser  
450 455 460

Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys  
465 470 475 480

Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu  
485 490 495

His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu  
500 505 510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
515 520 525

Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
530 535 540

Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
545 550 555 560

Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
565 570 575

Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
580 585 590

Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
595 600 605

Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
610 615 620

Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
625 630 635 640

Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
740 745 750

Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
900 905 910

Arg Tyr Arg  
915

<210> 35  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 35  
gtgaccctgg ttgtgaatac tcc 23

<210> 36  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 36  
acagccatgg tctatagctt gg 22

<210> 37  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 37  
gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38  
<211> 1813  
<212> DNA  
<213> Homo sapiens

<400> 38  
ggagccgccc tgggtgtcag cggctcggt cccgcgcacg ctccggccgt cgccgcagcct 60  
cggcacctgc aggtccgtgc gtcccgccgc tggcgccct gactccgtcc cggccaggga 120  
ggccatgat ttccctcccg gggccctgg tgaccaactt gctgcggttt ttgttccctgg 180  
ggctgagtgc cctcgcgcgc cccctcgccgg cccagctgca actgcacttg cccgccaacc 240  
ggttgcaggc ggtggagggaa gggaaagtgg tgcttccagc gtggtacacc ttgcacgggg 300  
agggtgtcttc atcccagcca tgggaggtgc cctttgtat gtggttttc aaacagaaaag 360  
aaaaggagga tcaggtgttg tcctacatca atggggtcac aacaagcaaa cctggaggat 420  
ccttggtcta ctccatgccc tcccgaaacc tgccttgcg gctggagggtt ctccaggaga 480  
aagactctgg cccctacagc tgctccgtga atgtcaaga caaacaaggc aaatctaggg 540  
gccacagcat caaaaacctta gaactcaatg tactggttcc tccagctccct ccattctgcc 600  
gtctccaggc tggcccccattt gtggggggcaaa acgtgaccct gagctgcccag tctccaaagga 660  
gtaagccgc tgccttgcattt cagtgccatc ggcagcttcc atcccttccag actttctttg 720  
caccagcatt agatgtcattt cgtgggtctt taagcctcactt caacctttcg tcttccatgg 780  
ctggagtcta tgccttgcattt gcccacaatg aggtgggcac tgcccaatgt aatgtgacgc 840  
tggaaagtggc cacaatctcc aagaatggga ccctttccattt tgccttgcattt ccattttcc 900  
ttggactggc gttgtggctt gggctggcc tcttgcattt cccgcggggc aaggccctgg 960  
aggagccagc caatgtatc aaggaggatg ccattgtcc cccggaccctt ccctggccca 1020  
agagctcaga cacaatctcc aagaatggga ccctttccattt tgccttgcattt ccattttcc 1080  
tccggccacc ccatggccctt cccaggccctt gtcatttgc cccacggccca agtcttccca 1140  
gccaggccctt gccccttgcattt cccaggccctt gtcatttgc cccacggccca agtcttccca 1200

cccccatccc tggtggggtt tcttcctctg gcttgagccg catgggtgct gtgcctgtga 1260  
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aaggatttgg ggtctctcct tccataagg gtcacctcta gcacagaggc ctgagtcatg 1380  
ggaaagagtc acactcctga cccttagtac tctgccccca cctctcttta ctgtggaaa 1440  
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attgggagga gcctccaccc acccctgact cctccttatg aagccagctg ctgaaattag 1560  
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ataacctgtc aggctggctt ggttaggtt tactggggca gaggataggg aatctctt 1740  
taaaaactaac atgaaatatg tgggttttc atttgc当地 ttaaataaaag atacataatg 1800  
tttgatgaa aaa 1813

<210> 39  
<211> 390  
<212> PRT  
<213> Homo sapiens

<400> 39  
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu  
1 5 10 15  
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln  
20 25 30  
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val  
35 40 45  
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln  
50 55 60  
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys  
65 70 75 80  
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro  
85 90 95  
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg  
100 105 110  
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val  
115 120 125  
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr  
130 135 140  
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu  
145 150 155 160  
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser  
165 170 175  
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro  
180 185 190  
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser  
195 200 205

Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys  
210 215 220

Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu  
225 230 235 240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly  
245 250 255

Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His  
260 265 270

Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp  
275 280 285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
370 375 380

Gln Ala Gly Ser Leu Val  
385 390

<210> 40  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 40  
agggtctcca ggagaaaagac tc 22

<210> 41  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 41	
attgtgggcc ttgcagacat agac	24
<210> 42	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 42	
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc	50
<210> 43	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 43	
gtgtgacaca gcgtggc	18
<210> 44	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 44	
gaccggcagg cttctgcg	18
<210> 45	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 45	
cagcagcttc agccaccagg agtgg	25
<210> 46	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 46  
ctgagccgtg ggctgcagtc tcgc

24

<210> 47  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 47  
ccgactacga ctggtttttc atcatgcagg atgacacacata tgtgc 45

<210> 48  
<211> 2822  
<212> DNA  
<213> Homo sapiens

<400> 48  
cgccaccact gcggccaccg ccaatgaaac gcctcccgct cctagtggtt ttttccactt 60  
tgttgaatttgc ttccctataact caaaatttgc ccaagacacc ttgtctccca aatgcaaaat 120  
gtgaaatacg caatggaaatttgc attgcaacat gggattttca ggaaatggtg 180  
tcacaatttgc tgaagatgtat aatgaatgtg gaaatttac tcagtcctgt ggcgaaaatg 240  
ctaatttgc acacacagaa ggaagtttattt attgtatgtg tgcacatggc ttccatgttcc 300  
gcagtaacca agacagggtt atcactaatg atgaaaccgt ctgtatagaa aatgtgaatg 360  
caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaaact ttaacaaaaaa 420  
tcagatccat aaaagaacact gtggcttgc tacaagaatg ctatagaaat tctgtgacag 480  
atctttcacc aacagatata attacatata tagaaatattt agctgaatca tcttcattttc 540  
tagttacaa gaacaacact atctcagcca aggacaccct ttcttaactca actcttactg 600  
aatttgtaaa aaccgtgaat aattttgttc aaagggatac attttagttt tgggacaagt 660  
tatctgtgaa tcataggaga acacatctt caaaactcat gcacactgtt gaacaagcta 720  
ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatataat tcaacggata 780  
tagctctcaa agttttcttt tttgatttcat ataacatgaa acatatttcat cctcatatga 840  
atatggatgg agactacata aatatatttca caaagagaaaa agctgcataat gattcaaatg 900  
gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcattttctt 960  
acaacttctt attgaaacactt caaaattatg ataatttcttga agaggaggaa agagtcataat 1020  
cttcagtaat ttcatgttca atgagctcaa acccaccac attatatgaa cttggaaaaaa 1080  
taacatttac attaagtcat cgaaaaggta cagataggtt taggagtctt tgcattttt 1140  
ggaatttactc acctgtatacc atgaatggca gctggcttc agagggtgtt gagctgacat 1200  
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gtgaaattca aaggccagg acaacaatttca acaaaaaatct ttgcgttgc ctattttctt 1440  
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tacatctcta tctcatttttgc tgggttgc tctacaacaa gggatttttgc cacaagaattt 1620  
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acagatatta tggcacaacc aagttatgtt ggcttagc acacacaaatcttttggatgg 1740  
gttttatagg accagcatgc ctaatcatttca ttgttcaatctt cttggcttttgc ggagtcataat 1800  
tatacaaagt ttttgcgttca actgcagggtt tgaaaccaga agtttagttgc tttgagaaca 1860  
taaggtcttgc tgcaagagga gcccctcgctc ttctgttccct tctcggcacc acctggatct 1920  
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atgcttcca gggatgttc atttttat tcctgtgt tttatctaga aagattcaag 2040  
aagaatatta cagattgttc aaaaatgtcc cctgtgtt tggatgttta aggtaaacat 2100  
agagaatggt ggataattac aactgcacaa aaataaaaat tccaagctgt ggatgaccaa 2160  
tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaaa agtattttaa 2220  
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acacgagaag tatatgaatg tcctgaagga aaccactggc ttgatattc tgtgactcgt 2460  
gttgcccttg aaactagtcc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520  
cataagagaa tgaagggca gaatatcaaa cagtggaaag ggaatgataa gatgtattt 2580  
gaatgaactg tttttctgt agactagctg agaaattgtt gacataaaaat aaagaattga 2640  
agaaacacat ttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700  
agacttctgt ttgctaaatc tggctttt tctaataattc taaaaaaaaaaa aaaaagggtt 2760  
acctccacaa attgaa 2820  
aa 2822

<210> 49  
<211> 690  
<212> PRT  
<213> Homo sapiens

<400> 49  
Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys  
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Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys  
20 25 30  
  
Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe  
35 40 45  
  
Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn  
50 55 60  
  
Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly  
65 70 75 80  
  
Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln  
85 90 95  
  
Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn  
100 105 110  
  
Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys  
115 120 125  
  
Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln  
130 135 140  
  
Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile  
145 150 155 160  
  
Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys  
165 170 175  
  
Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr  
180 185 190

Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val  
195 200 205

Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys  
210 215 220

Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe  
225 230 235 240

Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys  
245 250 255

Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met  
260 265 270

Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala  
275 280 285

Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser  
290 295 300

Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln  
305 310 315 320

Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile  
325 330 335

Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys  
340 345 350

Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser  
355 360 365

Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp  
370 375 380

Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser  
385 390 395 400

Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly  
405 410 415

Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln  
420 425 430

Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr  
435 440 445

Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys  
450 455 460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
675 680 685

Leu Arg  
690

<210> 50  
<211> 589  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (61)..(61)  
<223> a, t, c or g

<400> 50

tggaaaacata tcctccctca tatgaatatg gatggagact acataaaatat atttccaaag 60  
ngaaaaagccg gcatatggat tcaaatggca atgttgcagt tgcattttta tattataaga 120  
gtatttggtcc ctttgcttcc atcatctgac aacttcttat tggaaacctca aaatttatgtat 180  
aatttctgaag aggaggaaag agtcataatct tcagtaattt cagtctcaat gagctcaaac 240  
ccaccccacat tatatgaact tggaaaaata acatttacat taagtcatcg aaagggtcaca 300  
gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360

tggtcttcag agggctgtga gctgacatac tcaaatgaga cccacaccc 420  
aatcacctga cacatttgc aattttgatg tcctctggc cttccattgg tattaaagat 480  
tataatattc ttacaaggat cactcaacta ggaataatta tttcaactgat ttgtcttgcc 540  
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51  
gttaatgagc tccattacag 20

<210> 52  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52  
ggagtagaaa gcgcattgg 18

<210> 53  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53  
cacctgatac catgaatggc ag 22

<210> 54  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54  
cgagctcgaa ttaattcg 18

<210> 55  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
     oligonucleotide probe

<400> 55  
 ggatctcctg agtcagg 18

<210> 56  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
     oligonucleotide probe

<400> 56  
 cctagttgag tgatccttgt aag 23

<210> 57  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
     oligonucleotide probe

<400> 57  
 atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcatt 50

<210> 58  
 <211> 2137  
 <212> DNA  
 <213> Homo sapiens

<400> 58  
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 cgctaagcga ggcctccctcc tcccgcagat ccgaacggcc tggggcgggggt caccggct 120  
 gggacaagaa gccgcgcgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180  
 aggccgggtg tgagtgggtg tggcgggggg gcggaggcgtt gatgcaatcc cgataagaaa 240  
 tgctcgggtg tcttgggcac ctacccgtgg gggccgtaaag ggcgtactat ataaggctgc 300  
 cggcccgag cccgcgcgc gtcagagcag gagcgcgtgc tccaggatct agggccacga 360  
 ccatcccaac cccgcactca cagccccgca ggcgcattccg gtcgcgcgc acgcctccgc 420  
 acccccatcg cccggactgc gccgagagcc ccagggaggt gccatgcggc gcgggtgtgt 480  
 ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctcgc 540  
 ctctcggac gcggggccccc acgtgacta cggctgggc gaccccatcc gcctgcggc 600  
 cctgtacacc tccggccccc acgggccttc cagctgcttc ctgcgcatcc gtgccgacgg 660  
 cgtcgtggac tgcgcgcggg gccagagcgc gcacagttt ctggagatca aggcagtcgc 720  
 tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgcgc 780  
 cggcaagatg caggggctgc ttctactc ggaggaagac tggctttcg aggaggagat 840  
 cccgcgcgc ggcgcataatg tggaccgatc cgagaagcac cgcgcgcgc tctccctgag 900  
 cagtgccaaa cagcggcagc tggacaagaa cagaggctt cttccactct ctcatttcct 960  
 gcccgcgtc cccatggtcc cagaggagcc tgaggacctc agggggccact tggaaatctga 1020  
 catgttctct tcgccccctgg agaccgacag catggaccca tttggccttgc tcaaccggact 1080  
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tgctgccagg ggctgtggta cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200  
agtccacgtt ctgttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260  
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cagaagacag gcagtagttt taatttcagg aacaggtgat ccactctgtaa acacagcagg 1560  
taaatttcac tcaacccat gtgggaattt atctatatct ctacttccag ggaccattt 1620  
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cccaggcccc ccacctttagt tcaacctgca cttcttggc aaaaatcagg aaaagaaaaag 1920  
atttgaagac cccaagttct gtcaataact tgctgtgtgg aagcagcggg ggaagaccta 1980  
gaacccttcc cccagcactt ggtttccaa catgatattt atgagtaatt tattttgata 2040  
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<210> 59  
<211> 216  
<212> PRT  
<213> Homo sapiens

<400> 59  
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1 5 10 15  
  
Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
20 25 30  
  
His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
35 40 45  
  
Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
50 55 60  
  
Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
65 70 75 80  
  
Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
85 90 95  
  
Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
100 105 110  
  
Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Ile Arg Pro  
115 120 125  
  
Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
130 135 140  
  
Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
145 150 155 160  
  
Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 62

ccagtccgggt gacaagccca aa

22

<210> 63

<211> 1295

<212> DNA

<213> Homo sapiens

<400> 63

cccagaagtt caagggccccc cggcctcctg cgctcctgcc gccgggaccc tcgacccct 60  
cagagcagcc ggctgccccc ccgggaagat ggcgaggagg agccgccacc gcctccctcct 120  
gctgctgctg cgctacccctgg tggtcgcccct gggctatcat aaggcctatg ggtttctgc 180  
cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctattt tagcctgcaa 240  
aaccctaaag aagactgttt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300  
ctttgtctac tatcaacaga ctcttcaagg tgatttaaa aatcgagctg agatgataga 360

tttcaatatac cgatcaaaaa atgtgacaag aagtatgcg gggaaatatac gttgtgaagt 420  
tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgaaagtatt 480  
agtggctcca gcagttccat catgtgaagt accctttct gctctgagtg gaactgtggt 540  
agagctacga tgtcaagaca aagaaggaa tccagtcct gaatacacat ggtttaagga 600  
tggcatccgt ttgctagaaa atccagact tggctccaa agcaccaaca gctcatacac 660  
aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720  
atattcctgt gaagcccgca attctgttg atatgcagg tgcctggaa aacgaatgca 780  
agtagatgt ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
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gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020  
gttctagacc agtctggcca atatggtaa accccatctc tactaaaata caaaaattag 1080  
ctgggcatgg tggcatgtgc ctgcagttcc agtgcgttgg gagacaggag aatcacttga 1140  
acccgggagg cggaggttgc agttagctga gatcacgcca ctgcagtcga gcctggtaa 1200  
cagagcaaga ttccatctca aaaaataaaaa taaataataa aataaataact gtttttacc 1260  
tgtagaattc ttacaataaa tatacgatc tattc 1295

<210> 64  
<211> 312  
<212> PRT  
<213> Homo sapiens

<400> 64  
Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
1 5 10 15  
  
Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
20 25 30  
  
Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
35 40 45  
  
Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
50 55 60  
  
Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
65 70 75 80  
  
Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
85 90 95  
  
Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
100 105 110  
  
Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
115 120 125  
  
Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
130 135 140  
  
Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
145 150 155 160  
  
Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
165 170 175  
  
Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met

180	185	190
Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp		
195	200	205
Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg		
210	215	220
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile		
225	230	235
Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu		
245	250	255
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser		
260	265	270
Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn		
275	280	285
Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala		
290	295	300
Gly Gly Ser Arg Gly Gln Glu Phe		
305	310	

<210> 65  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 65  
atcgttgtga agtttagtgcc cc 22

<210> 66  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 66  
acctgcgata tccaaacagaa ttg 23

<210> 67  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

48

<210> 68

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 68

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gcatcatgct gctattcctg caaatactga agaagcatgg gatttaataa ttttacttct 180  
aaataaaatga attactcaat ctccatgac catctataca tactccacct tcaaaaagta 240  
catcaatatt atatcattaa ggaaatagta accttctt ctccaatatg catgacattt 300  
ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgggttcta 360  
tggcattcat catttgacaa atgcaagcat cttccttatac aatcagctcc tattgaactt 420  
actagcactg actgtggaat ccttaaggc ccattacatt tctgaagaag aaagctaaga 480  
tgaaggacat gccactccga attcatgtgc tactggcct agctatcact acactagtac 540  
aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttgg 600  
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<210> 69

<211> 708  
<212> PRT  
<213> Homo sapiens

<400> 69  
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Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
35 40 45  
Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
50 55 60  
Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn  
65 70 75 80  
Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
85 90 95  
Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
100 105 110  
Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
115 120 125  
Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
130 135 140  
Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
145 150 155 160  
Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
165 170 175  
Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
180 185 190  
Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
195 200 205  
Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
210 215 220  
Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
225 230 235 240  
Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
245 250 255  
Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
260 265 270  
Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu

	275	280	285												
Leu	Gly	Ile	Asn	Asn	Met	Pro	Glu	Leu	Ile	Ser	Ile	Asp	Ser	Leu	Ala
290						295					300				
Val	Asp	Asn	Leu	Pro	Asp	Leu	Arg	Lys	Ile	Glu	Ala	Thr	Asn	Asn	Pro
305					310				315				320		
Arg	Leu	Ser	Tyr	Ile	His	Pro	Asn	Ala	Phe	Phe	Arg	Leu	Pro	Lys	Leu
	325					330					335				
Glu	Ser	Leu	Met	Leu	Asn	Ser	Asn	Ala	Leu	Ser	Ala	Leu	Tyr	His	Gly
	340					345					350				
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn
	355					360					365				
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
	370					375				380					
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro
	385				390				395			400			
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
		405						410				415			
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu
		420					425					430			
Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala
		435					440				445				
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu
		450				455				460					
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
		465				470				475			480		
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys
			485					490			495				
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys
				500			505				510				
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys
				515			520				525				
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser
				530			535			540					
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr
			545				550			555			560		
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys
				565				570			575				
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys

580

585

590

Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn  
595 600 605

Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn  
610 615 620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

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agctgcagcc ttttgaaca ca gcaagaagg aaatcaatag tgtggacagg gctggAACCT 120  
ttaccacgct ttttggagta gatgaggaat gggctcgta ttatgctgac attccagcat 180  
gaatctggta gacctgtggta taacccgttc cctctccatg tgcctcctcc tacaaagttt 240  
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaaagggt gtctttgttc 300  
ttccctctggg gttttaatg tcacctgttag caatgcaaat ctcaaggaaa taccttagaga 360  
tcttcctcct gaaacagtct tactgtatct ggactccaat cagatcacat ctattccaa 420  
tgaatttttt aaggaccccttcc atcaacttgag agttctcaac ctgtccaaaaa atggcattga 480  
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttg 540  
cgacaatcggtt attcaaagtgc tgccaaaaaa tgccttcaat aacctgaagg ccagggccag 600  
aattgccaac aacccttggc actgcgactg tactctacag caagttctga ggagcatggc 660  
gtccaatcat gagacagccc acaacgtgtat ctgtaaaacg tccgtgttgg atgaacatgc 720  
tggcagacca ttccctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaaaac 780  
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cctgccaagc aggcagaaga aagcagatga acctgatgtat attagcactg tggatagtg 960  
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cacccttaa ttgtacccccc gatggtatat ttctgagtaa gctactatct gaacattatgt 1200  
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cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
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Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
245 250 255

Thr Val Val

<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaaacgctc aaccaggacg 300  
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<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

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20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys

35	40	45
Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala		
50	55	60
Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys		
65	70	75
80		
Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His		
85	90	95
Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro		
100	105	110
Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser		
115	120	125
Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn		
130	135	140
Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp		
145	150	155
160		
Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp		
165	170	175
Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser		
180	185	190
Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr		
195	200	205
Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His		
210	215	220
Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg		
225	230	235
240		
Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr		
245	250	255
Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His		
260	265	270
Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr		
275	280	285
Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly		
290	295	300
Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly		
305	310	315
320		
Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr		
325	330	335
Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu		

340

345

350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
370 375 380

Trp Arg, Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
435 440 445

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn  
580 585 590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser  
595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
610 615 620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 74  
tcacacctggag cctttattgg cc 22

<210> 75  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 75  
ataccagcta taaccaggct gcg 23

<210> 76  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 76  
caacagtaag tggtttgatg ctcttccaaa tcttagagatt ctgatgattg 50  
gg 52

<210> 77  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 77  
ccatgtgtct cctcctacaa ag 22

<210> 78  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 78  
ggaaatagat gtgatctgat tgg 23

<210> 79  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 79  
cacctgttagc aatgcaaatc tcaagggaaat accttagagat cttccctcctg 50

<210> 80  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 80  
agcaaccgcgc tgaagctcat cc 22

<210> 81  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 81  
aaggcgcggt gaaagatgt a gacg 24

<210> 82  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 82  
gactacatgt ttcaggaccc t tacaaccc tc aagtca ctgg aggttggcga 50

<210> 83  
<211> 1685  
<212> DNA  
<213> Homo sapiens

<400> 83  
cccacgcgtc cgcacccctcg ccccgccgtc cgaagcggtc cggggggcc ctttcggtca 60  
acatcgtagt ccacccccc tc cccatcccc a gccccgggg attcaggctc gccagcgccc 120  
agccaggag ccggccggga a g c g c g a t g g g g c c c a g c c g c t c t g c t c t g c 180

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aaaca						1685

<210> 84

<211> 398

<212> PRT

<213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala  
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Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
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Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
385 390 395

<210> 85  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 85  
gcttaggaatt ccacagaagc cc 22

<210> 86  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 86  
aaccttggaat gtcaccgagc tg 22

<210> 87  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 87  
cctagcacag tgacgaggga cttggc 26

<210> 88  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 88  
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 89  
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90  
<211> 2755  
<212> DNA

<213> Homo sapiens

<400> 90

gggggttagg gaggaaggaa tccaccccca cccccccaaa ccctttctt ctccttcct 60  
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gctgttaatt tggatgaga tcggggatga attgctcgct taaaaatgc tgcttggat 180  
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr			
35	40	45	
Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe			
50	55	60	
Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn			
65	70	75	80
Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu			
85	90	95	
Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His			
100	105	110	
Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly			
115	120	125	
Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp			
130	135	140	
Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile			
145	150	155	160
Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr			
165	170	175	
Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu			
180	185	190	
Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu			
195	200	205	
Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys			
210	215	220	
Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val			
225	230	235	240
Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr			
245	250	255	
Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro			
260	265	270	
Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr			
275	280	285	
Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala			
290	295	300	
Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg			

305	310	315	320
Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala			
325	330	335	
Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly			
340	345	350	
Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala			
355	360	365	
Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp			
370	375	380	
Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn			
385	390	395	400
Leu Ile Leu Leu Asp Leu Gly Asn Asn Ile Ala Thr Val Glu Asn			
405	410	415	
Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser			
420	425	430	
Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn			
435	440	445	
Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro			
450	455	460	
Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn			
465	470	475	480
Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu			
485	490	495	
Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala			
500	505	510	
Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly			
515	520	525	
Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala			
530	535	540	
Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr			
545	550	555	560
Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu			
565	570	575	
Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His			
580	585	590	
Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser			
595	600	605	
Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu			

610 615 620  
Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
625 630 635 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
645 650 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr  
660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
690 695

<210> 92  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 92  
gttggatctg ggcaacaata ac 22

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 93  
attgttgtgc aggctgagtt taag 24

<210> 94  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 94  
ggtggtata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95  
<211> 2226  
<212> DNA  
<213> Homo sapiens

<400> 95

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
1 5 10 15

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val

50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
65 70 75 80

Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln  
340 345 350

Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala

355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380 '
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
400		
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
480		
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	

<210> 97  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 97  
tggaaggaga tgcgatgcca cctg 24

<210> 98  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 98  
tgaccagtgg ggaaggacag 20

<210> 99  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 99  
acagagcaga ggggccttg 20  
  
<210> 100  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe  
  
<400> 100  
tcagggacaa gtgggtctc tccc 24  
  
<210> 101  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe  
  
<400> 101  
tcagggaaagg agtgtgcagt tctg 24  
  
<210> 102  
<211> 50  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe  
  
<400> 102  
acagctcccg atctcagttt cttgcattgc ggacgaaatc ggcgctcgct 50  
  
<210> 103  
<211> 2026  
<212> DNA  
<213> Homo sapiens  
  
<400> 103  
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tatccccccgg ctacctgggc cgccccgcgg cggtgcgcgc gtgagaggga ggcgcgggc 180  
agccgagcgc cggtgtgagc cagcgctgct gccagtgtga gcggcggtgt gagcgcgggtg 240  
ggtgccggagg ggcgtgtgtg ccggcgccgcg cgccgtgggg tgcaaaccgg ggcgtctac 300  
gctgccatga ggggcgcgaa cgccctggcgcc caactctgcc tgctgctggc tgccgccacc 360  
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ggagagtctg gatttattgg cagtgaaggt tttcctggag tgcgtcccttcc aaatagcaaa 480  
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gtgttatttgc ttgcacccttc aagccttgc cctgaggtgt tacaatcttgc tcttgcgttt 1980  
tctaaatcaa tgcttaataa aatatttta aaggaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala  
1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr  
20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly  
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr  
50 55 60

Val Pro Glu Gly Lys Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala  
340 345 350

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro  
355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu  
370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys  
385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys  
405 410 415

<210> 105  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
     oligonucleotide probe

<400> 105  
 ccgattcata gacctcgaga gt 22

<210> 106  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
     oligonucleotide probe

<400> 106  
 gtcaaggagt cctccacaat ac 22

<210> 107  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
     oligonucleotide probe

<400> 107  
 gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45

<210> 108  
 <211> 1838  
 <212> DNA  
 <213> Homo sapiens

<400> 108  
 cggacgcgtg ggcggacgcg tggcgcccc acggcgccc cgggctgggg cggtcgcttc 60  
 ttccttctcc gtggcctacg agggtccccca gcctggtaa agatggccccc atggccccc 120  
 aaggccctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180  
 atctggctcc agccctctcc acctcccccag tcttctcccc cgcctcagcc ccatccgtgt 240  
 catacctgcc ggggactgggt tgacagctt aacaagggcc tggagagaac catccggac 300  
 aactttggag gtggaaacac tgcctggag gaagagaatt tgtccaaata caaagacagt 360  
 gagaccgcgc tggtagaggt gctggagggt gtgtcagca agtcagactt cgagtgccac 420  
 cgccctgtgg agctgagtga ggagctgggt gagagctgggt ggtttcacaa gcagcaggag 480  
 gccccggacc tcttccagtg gctgtcgtca gattccctga agctctgctg ccccgccaggc 540  
 accttcgggc cctcctgcct tcctgtcct gggggaaacag agaggccctg cggtggtac 600  
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 tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720  
 agccatctgg tatgttcggc ttgtttggc ccctgtgccc gatgctcagg acctgaggaa 780  
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 ggctcctatg agtgccgaga ctgtgccaag gcctgcctag gctgcattgg ggcaggggcca 960  
 ggtcgctgtg agaagtgttag ccctggctat cagcaggtgg gctccaagtg tctcgatgtg 1020  
 gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtaaaaa caccgaggcgc 1080  
 ggttatcgct gcatctgtgc cgaggcgtac aagcagatgg aaggcatctg tgtgaaggag 1140  
 cagatcccgag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggcgtg 1200

cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taagggcgac 1260  
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gagcgcagt accgtgtgct ggagggctt atcaaggca gataatcgac gccaccac 1380  
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caggacagct tggtttattt ttgagagttgg gtaagcacc cctacctgcc ttacagagca 1500  
gcccgaggta ccaggcccg gcaagacaagg cccctgggggt aaaaagtagc cctgaagggt 1560  
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tgttcaccac atccccacac cccattgccca cttatttattt catctcagga aataaaagaaa 1800  
ggtctggaa agttaaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly  
1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser  
20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr  
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile  
50 55 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys  
180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
355 360 365

Met Phe Phe Gly Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
405 410 415

Ile Lys Gly Arg  
420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1461)..(1461)

<223> a, t, c or g

<400> 113

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aaagtccctcc accaccactc tggacctaag acctggggtt aagtgtgggt tgtgcatccc 1560  
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<210> 114  
<211> 366  
<212> PRT  
<213> Homo sapiens

<400> 114  
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20 25 30  
Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
35 40 45  
Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
50 55 60  
Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
65 70 75 80  
Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
85 90 95  
His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
100 105 110  
Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
115 120 125  
Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
130 135 140  
Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
145 150 155 160  
Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
165 170 175  
Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
180 185 190  
Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
195 200 205  
Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
210 215 220  
Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
225 230 235 240  
Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 115

aggactgcca taacttgccct g 21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc 22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118  
<211> 1857  
<212> DNA  
<213> Homo sapiens

<400> 118  
gtctgttccc aggagtcctt cggcggtgt tgggtcgtgc gcctgatcgc gatggggaca 60  
aaggcgcaag tcgagaggaa actgttgc ctcttcataat tggcgatcct gttgtctcc 120  
ctggcattgg gcaggttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180  
aatcctgtga agttgtcctg tgctactcg ggctttctt ctccccgtgt ggagtggaaag 240  
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300  
gaggaccggg tgaccttctt gccaactggt atcacctca agtccgtgac acggaaagac 360  
actgggacat acactgtat ggtctctgag gaaggcgca acagctatgg ggaggtaag 420  
gtcaagctca tcgtgcttgc gcctccatcc aagcctacag ttaacatccc ctccctgtcc 480  
accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540  
tacacctggt tcaaagatgg gatagtgtat cctacgaatc ccaaaggcac ccgtgccttc 600  
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtttga tccctgtca 660  
gcctctgata ctggagaata cagctgttag gcacggaaatg ggtatggac acccatgact 720  
tcaaattgtcg tgcgcattgg agctgtggag cggaatgtgg ggtcatcg ggcagccgtc 780  
cttgcataacc tgattcttgc gggatcttgc tgggtttgc ctataccgaa 840  
ggccactttg acagaacaaa gaaaggact tcgagtaaga aggtgattt cagccagcct 900  
agtgcggaa gtgaaggaga attcaaacag acctcgtcat tcctgggtgt agcctggtcg 960  
gctcaccgccc tatcatctgc atttgcctt ctcaggtgct accggactct ggccctgtat 1020  
gtctgttagtt tcacaggatg ccttatttgc tttctacacc ccacagggcc ccctacttct 1080  
tcggatgtgt ttttataat gtcagctatg tgcccatcc tccttcatgc cctccctccc 1140  
tttccatcca ctgctgatgt gcctgaaact tggtaaaatg gtttattccc catttcttgc 1200  
agggatcagg aaggaatcct gggatggca ttgacttccc ttctaagtag acagcaaaaa 1260  
tggcgggggt cgccaggaaatc tgcactcaac tgcccacctg gctggcaggatc ttttgc 1320  
aggatcttgc agcttgggttc tgggttttgc cttgtgtac tgacgaccag ggccagctgt 1380  
tctagagcgg gaatttagagg cttagagcggc tggaaatgggt gtttggat gacactgggg 1440  
tccttcatc tctggggccc actcttttgc tgggttttgc gggaaatgggtt gacactgggg 1500  
ctctgcccgt tccttcatttgc tacaagctga ctgacatttgc tgggttttgc gggaaatgggtt 1560  
agcttgcgtt gtggagagca tagtaaaatgc tcaagaaact tggaaatgggtt gggaaatgggtt 1620  
accgctgctc taaagaaaaaa aaaactggag gctggcgcgc tgggttttgc cctgtatcc 1680  
cagaggctga ggcaggcggc tcacacttgc tgggttttgc gggaaatgggtt gggaaatgggtt 1740  
ggagaaaaacc tactggaaat acaaagtttgc tgggttttgc tgggttttgc tgggttttgc 1800  
agctgctc tggcgcgc tgggttttgc acaagagcaaa aactccagct caaaaaaaaaaa aaaaaaaaaa 1857

<210> 119  
<211> 299  
<212> PRT  
<213> Homo sapiens

<400> 119  
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15  
  
Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30  
  
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45  
  
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80  
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95  
 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly  
 245 250 255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295  
 <210> 120  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
 <400> 120  
 tcgcggagct gtgttctgtt tccc

<210> 121  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 121  
tgatcgcgat ggggacaaag gcgcaggctc gagaggaaac tgttgtgcct 50

<210> 122  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 122  
acacctgggtt caaagatggg 20

<210> 123  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 123  
taggaagagt tgctgaaggc acgg 24

<210> 124  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 124  
ttgccttact caggtgtac 20

<210> 125  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 125  
 actcagcagt ggttagaaag 20

<210> 126  
 <211> 1210  
 <212> DNA  
 <213> Homo sapiens

<400> 126  
 cagcgcgtgg ccggcgccgc tgtgggaca gcatgagcgg cggtggatg ggcgcagggtt 60.  
 gaggcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120  
 gcctggaggc cgccgcgagc ccgccttcca ccccgaccc tcggccaggcc gcaggccca 180  
 gctcaggctc gtgcccaccc accaagttcc agtgcgcac cagtgctta tgcgtgcccc 240  
 tcacacctggcg ctgcgacagg gacttggact gcaagcgatgg cagcgatgag gaggagtgc 300  
 ggattgagcc atgtacccag aaagggaat gcccacccgc ccctggcctc ccctggccct 360  
 gcaccggcgt cagtgactgc tctggggaa ctgacaagaa actgcgcacac tgcagccg 420  
 tggcctgcct agcaggcgag ctccgtgca cgctgagcga tgactgcatt caactcacgt 480  
 ggcgcgtgcga cggccaccca gactgtcccg actccagcga cgagctcggc tggaaacca 540  
 atgagatcct cccggaaaggg gatgcaccaa ccatggggcc ccctgtgacc ctggagagt 600  
 tcacacctctc caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgcctcc 660  
 ctgtcgggaa tgccacatcc tcctctgccc gagaccagtc tggaaaccca actgcctatg 720  
 gggttattgc agctgctgcg gtgctcagtg caaggctggt caccggcacc ctccctcc 780  
 tggcctggct ccgagcccgag gaggcgcctcc gcccactggg gttactggtg gccatgaagg 840  
 agtccctgct gctgtcagaa cagaagaccc cgcgcctcg aggacaagca cttgccacca 900  
 ccgtcactca gcccctggcg tagccggaca ggaggagagc agtgcgcgg atgggtaccc 960  
 gggcacacca gcccctcagag acctgagttc ttctggccac gtggaaaccc tcggccg 1020  
 tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080  
 agcttaggatg gggAACCTGC cacagccaga actgaggggc tggcccccagg cagctccac 1140  
 gggtagaaac gcccctgtgc ttaagacact ccctgctgccc ccgtctgagg gtggcgattt 1200  
 aagttgcttc 1210

<210> 127  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<400> 127  
 Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
 1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
 20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
 35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
 50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
 65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
 85 90 95

Lys Gly Gln Cys Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
 100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
130 135 140 160

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala  
225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln  
245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 129

ttggttccac agccgagctc gtcg

24

<210> 130  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 130  
gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgcccacc 50

<210> 131  
<211> 1843  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1837)..(1837)  
<223> a, t, c or g

<400> 131  
cccacgcgtc cggctcgct cgctcgca gcggcgca cagaggtcgc gcacagatgc 60  
gggttagact ggcgggggga ggaggcggag gaggaaagga agctgcgtc atgagaccca 120  
cagactcttgc caagctggat gcctctgtg gatgaaagat gtatcatgga atgaacccga 180  
gcaatggaga tggatttcta gaggcagcgc agcagcagca gcaacctcag tccccccaga 240  
gactcttggc cgtgatcctg tggttcagc tggcgctgtg cttcgccct gcacagctca 300  
cggcggtt cgatgacctt caagtgtgt ctgaccccg cattcccgag aatggcttca 360  
ggaccccccag cggagggtt ttcttgaag gctctgtac ccgatttac tgccaagacg 420  
gattcaagct gaaggcgct acaaagagac tggtttcaa gcattttat ggaaccctag 480  
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540  
aagatgctga gattcataac aagacatata gacatggaga gaagctaattc atcacttgc 600  
atgaaggatt caagatccgg taccggacc tacacaatat ggtttcatta tgtcgcgt 660  
atgaaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
atggctatgt aaacatctct gagctccaga cctcctccccc ggtggggact gtgatctcct 780  
atcgctgctt tcccgattt aaacttgtat ggtctgcgtt tcttgagtgc ttacaaaacc 840  
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgcactac 900  
ctccaatggt gagtcacgga gatttcgtct gccacccgcg gccttgcgtgc cgctacaacc 960  
acgaaactgt ggtggagttt tactgcgtc ctggctacag cctcaccaggc gactacaagt 1020  
acatcacctg ccagtatgga gagggttcc tttttatca agtctactgc atcaaattcg 1080  
agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaaagatt gtggcggtca 1140  
cgccaaccag tggctgtgtc gtgctgtgc tcgtcatcct ggccaggatg ttccagacca 1200  
agttcaaggc ccactttccc cccagggggc ctcccccggag ttccagcagt gaccctgact 1260  
ttgtgggtgtt agacggcggtc cccgtcatgc tcccgctcta tgacgaagct gtgagtggcg 1320  
gttggatgtc cttggggcc ggttacatgg cctctgtggg ccagggtgc cccttacccg 1380  
tggacgacca gagcccccca gcataccccc gctcaggggc cacggacaca gggccagggg 1440  
agttagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500  
ctcccagggtc ccaagagagc acccaccctg ctgcggacaa ccctgacata attgcccagca 1560  
cgccagagga ggtggcatcc accagccca gcatccatca tgcccactgg gtgttgc 1620  
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctt tcaaatacat 1680  
gttggatgtc ggagttgatt ctttccttc tcttggttt agacaaatgt aaacaaagct 1740  
ctgtatccttta aaattgttat gctgatagag tggtgaggc tgaaagcttgc atcaagtcc 1800  
gttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490  
<212> PRT  
<213> Homo sapiens

<400> 132  
Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
1 5 10 15  
Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
20 25 30  
Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
35 40 45  
Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
50 55 60  
Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
65 70 75 80  
Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
85 90 95  
Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
100 105 110  
Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
115 120 125  
Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
130 135 140  
Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
145 150 155 160  
Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
165 170 175  
Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn  
180 185 190  
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr  
195 200 205  
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys  
210 215 220  
Leu Gln Asn Leu Ile Trp Ser Ser Pro Pro Arg Cys Leu Ala Leu  
225 230 235 240  
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe  
245 250 255  
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val  
260 265 270  
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr

275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
320		
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
400		
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460
Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His		
465	470	475
480		
His Ala His Trp Val Leu Phe Leu Arg Asn		
485	490	

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 133

atctcctatc gctgcttcc cg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134  
 agccaggatc gcagtaaaac tcc

23

<210> 135  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135  
 atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct

50

<210> 136  
 <211> 1815  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggccgtcg gtggcctaga 60  
 gatgctgctg ccgcgggtgc agttgtcgcg cacgcctctg cccgcgcagcc cgctccaccg 120  
 ccgttagcgcc cgagtgtcggt ggggcgcacc cgagtcgggc catgaggccg gaaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgcacg gtcgcctgc 240  
 ttagtgcctc ggatttggac ctcagaggag ggcagccagt ctgcgggga gggacacaga 300  
 ggcctgtta taaagtctt tacttccatg atacttctcg aagactgaac tttgaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agcttagtcg catcgagtct gaagatgaac 420  
 agaaaactgtat agaaaagttc attgaaaacc tcttgcatt ttagtgcac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagg ctgcaggac ctttatgctt 540  
 ggactgtatgg cagcatatca caatttaga actggtatgt ggatgagccg tcctgcggca 600  
 gcgaggctcg cgtggcatg taccatcagc catcggcacc cgctggcatc ggaggccct 660  
 acatgttcca gtggaatgtat gaccggtgca acatgaagaa caatttcatt tgcaaataatt 720  
 ctgatgagaa accagcagtt cttcttagag aagctgaagg tgagggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccctt ctccctctcc 900  
 ttgtggtcac cacagttgtat tggtgggtt ggatctgtat aaaaagaaaa cggggcagc 960  
 cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag gaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcgaa agctgactta gctgagaccc 1080  
 ggccagacct gaagaatatt tcattccggat tgggttcggg agaagccact cccgatgaca 1140  
 tgtctgtat ctagacaac atggctgtat accatcaga aagtgggtt gtgactctgg 1200  
 tgagcgttga gaggatgtt gtcataatg acatttatgt gttccccca gaccaatagg 1260  
 ggaggatgtt ggtctgttga tgggtggaaa atgaaatata tggttattag gacatataaa 1320  
 aaactgaaac tgacaacaat gggaaaagaaaa tgataagcaa aatcccttta ttttctataa 1380  
 ggaaaatatac cagaagggtct atgaaacaaatg ttagatcagg tcctgtggat gagcatgtgg 1440  
 tccccacgac ctccctgttgg acccccacgt tttggctgtat tccttccatcc cagccagtc 1500  
 tccagctcgat ccttatgaga aggtacccgtt cccagggtctg gcacatagta gagtctcaat 1560  
 aaatgtcact tgggtgggtt tatctaactt ttaaggggaca gagcttacc tggcgtgtat 1620  
 aaagatgggc tgggtggatgtt gggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atttatcat acagacagaa aatccagaat cttttcaaaag cccacatatg gtagcgcacagg 1740  
 ttggcctgttgc catcggtcaat tctcatatct gttttttca aagaataaaa tcaaataaa 1800  
 agcaggaaaa aaaaaa

1815

<210> 137  
<211> 382  
<212> PRT  
<213> Homo sapiens

<400> 137  
Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15  
  
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30  
  
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45  
  
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60  
  
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80  
  
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95  
  
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110  
  
Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
115 120 125  
  
Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
130 135 140  
  
Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
145 150 155 160  
  
Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
165 170 175  
  
Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
180 185 190  
  
Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
195 200 205  
  
Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
210 215 220  
  
Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
225 230 235 240  
  
Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
245 250 255  
  
Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
260 265 270

Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
275 280 285

Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
290 295 300

Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
305 310 315 320

Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
325 330 335

Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
340 345 350

Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
355 360 365

Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
370 375 380

<210> 138

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 138

gttcattgaa aacctttgc catctgatgg tgacttctgg attgggctca 50

<210> 139

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 139

aagccaaaga agcctgcagg aggg 24

<210> 140

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 140

cagtccaagc ataaagggtcc tggc 24

<210> 141  
<211> 1514  
<212> DNA  
<213> Homo sapiens

<400> 141  
gggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
gcatccgcag gttccgcgg acttggggc gcccgcgtag ccccgccgcg cgcagaagac 120  
ttgtgtttgc ctccctgcagc ctcaaccggc agggcagcga gggcctacca ccatgatcac 180  
tgggtgttc agcatgcgtc tggtggccccc agtgggcgtc ctgacctcg tggctactg 240  
cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccgg 300  
cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcggt tttcgacacg gggctcgag 360  
tcctctcaag cgcgtccgc tgaggagca ggtagagtgg aaccccccagc tattagaggt 420  
cccaccccaa actcagttt attacacagt caccaatcta gctgggtggc cgaaaccata 480  
ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctggca 540  
gctgaccaag gtgggcattgc agcaaatgtt tgccctggga gagagactga ggaagaacta 600  
tgtgaagac attcccttac ttccaccaac cttcaaccca caggaggtct ttattcggtc 660  
cactaacatt ttccggaaatc tgtagtccac ccgttggggc ctggctggc tttccagtg 720  
tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatcc 780  
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840  
tttacagcca ggaatctcag aggattgaa aaaggtgaag gacaggatgg gcattgacag 900  
tagtgataaa gtggacttct tcacccctcct ggacaacgtg gctgcccggc aggcacacaa 960  
cctcccaagc tgccccatgc tgaagagatt tgacccgtatc atcgaacaga gagctgtgga 1020  
cacatccttac tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080  
attcctccac atccttagaga gcaacctgct gaaagccatg gactctgcca ctgccccca 1140  
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
gaccctgggg attttggacc acaaatggcc accgttgcgtt gttgacctga ccatggaact 1260  
ttaccagcac ctggaaatcta aggagtgggt tttgcagtc tattaccacg ggaaggagca 1320  
ggtagccgaga ggttgcctg atgggcctg cccgctggac atgttcttgc atgcccattgc 1380  
agtttataacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440  
agttggaaat gaagagtaac tgatttataa aagcaggatg tggtgatttt aaaataaaagt 1500  
gccttataac aatg 1514

<210> 142  
<211> 428  
<212> PRT  
<213> Homo sapiens

<400> 142  
Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val  
1 5 10 15  
  
Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala  
20 25 30  
  
Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu  
35 40 45  
  
Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro  
50 55 60  
  
Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu  
65 70 75 80  
  
Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu  
85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu  
100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly  
115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val  
130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe  
145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu  
165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile His  
180 185 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
195 200 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
210 215 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
225 230 235 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
245 250 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
260 265 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
275 280 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
290 295 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
305 310 315 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
325 330 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
340 345 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
355 360 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
370 375 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
385 390 395 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
420 425

<210> 143  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143  
ccaactacca aagctgctgg agcc 24

<210> 144  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144  
gcagctctat taccacggga agga 24

<210> 145  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145  
tccttcccggt ggtaatagag ctgc 24

<210> 146  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146  
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147  
<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctccctttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttggcatg gctctgctat tctccttgat 120  
ccttgcatt tgccaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtgg 180  
gggcctccac cgctgtgaag ggcgggtgga ggtggAACAG aaaggccagt gggcaccgt 240  
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgtt tgccgggagc tggctgtgg 300  
agctgccagc ggaacccta gtggatttt gtatgagcca ccagcagaaa aagagcaaaa 360  
ggtcctcattt caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420  
agaagaagtt tatgattgtt cacatgatga agatgctgg gcacatgtgt agaaccaga 480  
gagcttttc tccccagttcc cagagggtgt caggctggct gacggccctg ggcattgcaa 540  
gggacgcgtg gaagtgaagc accagaacca gtggatacc gtgtgccaga caggctggag 600  
cctccggcc gcaaagggtgg tggccggca gctggatgt gggaggcgt tactgactca 660  
aaaacgctgc aacaagcatg cctatggccg aaaaccatc tggctgagcc agatgtcatg 720  
ctcaggacga gaagcaaccc ttcaaggattt cccttctggg ccttggggga agaacacctg 780  
caaccatgat gaagacacgt ggtcgaatg tgaagatccc ttgacttga gacttaggg 840  
aggagacaac ctctgctctg ggcgacttgg ggtgctgcac aaggcgtat gggctctgt 900  
ctgtgatgac aactggggag aaaaggagga ccaggtggta tgcaagcaac tggctgtgg 960  
gaagtccctc tctccctcct tcagagaccg gaaatgctat ggcctgggg ttggccgcatt 1020  
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attttggggg ttgcacactt gcacccacca ggaagatgtg gctgtcatct gctcgtgt 1140  
ggtggcattt atctaattctg ttgagtgccct gaatagaaga aaaacacaga agaaggggagc 1200  
atttactgtc tacatgactg catggatga acactgatct tcttctgcc ttggactggg 1260  
acttatactt ggtgcctctg atttcaggc cttcagagtt ggatcagaac ttacaacatc 1320  
aggtagttt ctcagggcat cagacatagt ttgaaactac atcaccaccc ttccatgtc 1380  
tccacattgc acacagcaga ttcccagccct ccataattgt gtgtatcaac tacttaata 1440  
cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccattgtcc 1500  
tgtttctctg aagaactctg aaaaaataca gattttggta ctgaaagaga ttctagagga 1560  
acgaaatttt aaggataaaat ttctgaatt ggttatgggg ttctgaaat tggctctata 1620  
atctaatttag atataaaattt ctggtaactt tatttacaat aataaagata gcactatgtg 1680  
ttcaaa 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Asp Asn Leu Cys Ser Gly Arg  
245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 149	
ttcagctcat cacttcacc tgcc	24
<210> 150	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 150	
ggctcataca aaataccact aggg	24
<210> 151	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 151	
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt	50
<210> 152	
<211> 1427	
<212> DNA	
<213> Homo sapiens	
<400> 152	
actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60	
accacacgcgt ccgcggacgc gtggggcggac gcgtggccg gctaccagga agagtctgcc 120	
gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180	
cctgggcgtc ttccggctct tccggctgct gcagtgggtg cgcgggaagg cctacctgctg 240	
aatgtctgtg gtgggtatca caggcgccac ctcagggctg ggcaaagaat gtgaaaaagt 300	
cttctatgct gcgggtgctt aactgggtct ctgtggccgg aatgggtggg ccctagaaga 360	
gctcatcaga gaacttaccg ctctcatgc caccaagggtg cagacacaca agccttactt 420	
gtgtacccctc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480	
gtgtttggc tatgtcgaca tacttgtcaa caatgtggg atcagctacc gtggtaccat 540	
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggccctagt 600	
tgctctaacc aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660	
catcagcagc atccaggcga agatgagcat tcctttcga tcagcatatg cagcctccaa 720	
gcacgcaacc caggctttct ttgactgtct gcgtggccgag atgaaacagt atgaaattga 780	
ggtagccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccatcaccgc 840	
ggatggatct aggtatggag ttatggacac caccacagcc caggccgaa gcccctgtgga 900	
ggtagggccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960	
cttactgcct tccttggtct tttatcttcg aactctggct cctgggctct tcttcagcct 1020	
catggcctcc agggccagaa aagagcggaa atccaagaac tccttagtact ctgaccagcc 1080	
agggccaggg cagagaagca gcactcttag gcttgcctac tctacaagg acagttgcat 1140	
ttgttgagac tttaatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200	
gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttctcc cagggtgagg 1260	
ggaaacactt aaggaataaa tatggagctg gggtaaca ctaaaaacta gaaataaaca 1320	
tctcaaacag taaaaaaaaaaa aaaaaaggc ggccgcgact ctagagtcga cctgcagaag 1380	

cttggccgccc atggcccaac ttgtttattt cagcttataa tggttac 1427

<210> 153  
<211> 310  
<212> PRT  
<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly  
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala  
100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr  
210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
225 230 235 240

Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val

260

265

270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
290 295 300

Arg Lys Ser Lys Asn Ser  
305 310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 154

ggtgctaaac tggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156

tcatactgtt ccatctcgac acgc

24

<210> 157

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157

aatgggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158

<211> 1771

<212> DNA

<213> Homo sapiens

<400> 158

cccacgcgtc cgctgggtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacacccaaa cgctcgcagc cacaaggatggc atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agcttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacacgc tgccaaatgc aaggactgg gtgccaaggt 360  
tcatacctt gtggtagact gcagcaacccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtattt agtaaataat gctggtagtgc tctatacatc 480  
agattgttt gctacacaag atcctcagat tgaaaagact tttgaagttt atgtacttgc 540  
acatttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggcccc ttcttactgg cttactgttc 660  
aagaagttt gctgctgtt gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaaacaa catgtctgtt tcctaattt gtaaacactg gcttcataa 780  
aaatccaagt acaagttgg gacccactct ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgtat ttttattcca tcttctatag cttttttaac 900  
aacattggaa aggatccctc ctgagcgtt cctggcagtt ttaaaacgaa aaatcagtgt 960  
taagttttagt gcagttttagt gatataaaat gaaagcgaa taagcaccta gttttctgaa 1020  
aactgatttta ccaggttttag gttgatgtca tctaatacgat ccagaattttt aatgtttgc 1080  
cttctgtttt ttctaattt cccatttct tcaatatcat ttttgaggct ttggcagtct 1140  
tcatttacta ccacttgc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
tacctttaga ggtgacttta agaaaaatga agaaaaagaa caaaaatgac tttttaaaaa 1260  
taatttccaa gattatttgc ggtcacctg aaggcttgc aaaatttgc ccataaccgt 1320  
ttatattaaca tatatttttgc ttttgatttgc cacttaaattt ttgtataattt tttgtttctt 1380  
tttctgttct acataaaatc agaaaacttca agctctctaa ataaaaatgaa ggactatatac 1440  
tagtggattt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500  
gccactctgt ttccctgagag atacctcaca ttccaaatgcc aaacatttct gcacaggaa 1560  
gctagaggtg gatacacgtg ttgcaagtat aaaagcatca ctgggatttgc aggagaattt 1620  
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1771

<210> 159

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Pro Leu Leu Ile Val  
1 5 10 15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
 65 70 75 80  
 Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
 85 90 95  
 Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
 100 105 110  
 Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
 115 120 125  
 Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
 130 135 140  
 Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr  
 145 150 155 160  
 Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
 165 170 175  
 Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
 180 185 190  
 Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
 195 200 205  
 Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
 210 215 220  
 Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
 225 230 235 240  
 Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
 245 250 255  
 Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
 260 265 270  
 Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
 275 280 285  
 Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
 290 295 300  
 <210> 160  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
 <400> 160  
 ggtgaaggca gaaattggag atg

<210> 161  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 161  
atcccatgca tcagcctgtt tacc 24

<210> 162  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 162  
gctgggttag tctatacatc agatttgttt gctacacaag atcctcag 48

<210> 163  
<211> 2076  
<212> DNA  
<213> Homo sapiens

<400> 163  
cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgccgc 60  
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttgggtccat gtggaaagggtg 120  
atgtttcgc tggcctgtt gatgcctggc ccctgtatg ggctgtttcg ctccctatac 180  
agaagtgttt ccatgccacc taaggagac tcaggacagc cattatttct cacccttac 240  
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttccagga 300  
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360  
ttcttcttgt tcttcccagc tcagatacag ccagaagatg ccccaagtatg tctctggcta 420  
cagggtgggc cgggaggatcc atccatgtt ggactcttg tggaaacatgg gccttatgtt 480  
gtcacaagta acatgacctt gcgtgacaga gacttccct ggaccacaac gctctccatg 540  
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gcagtcaatg aggacgatgt agcacggat ttatacagtg cactaattca gttttccag 660  
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gaaataaaaaa tattatataat aaaagtaaaa aaaaaa 2076

<210> 164  
<211> 476  
<212> PRT  
<213> Homo sapiens

<400> 164  
Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
1 5 10 15  
  
Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
20 25 30  
  
Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
35 40 45  
  
Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
50 55 60  
  
Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val  
65 70 75 80  
  
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln  
85 90 95  
  
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro  
100 105 110  
  
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val  
115 120 125  
  
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr  
130 135 140  
  
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser  
145 150 155 160  
  
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala  
165 170 175  
  
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu  
180 185 190  
  
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys  
195 200 205  
  
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg  
210 215 220

Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser  
225 230 235 240

Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile  
245 250 255

Gly Leu Leu Asp Glu Lys Gln Lys Tyr Phe Gln Lys Gln Cys His  
260 265 270

Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu  
275 280 285

Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr  
290 295 300

Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys  
305 310 315 320

Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro  
325 330 335

Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly  
340 345 350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165  
ttccatgcc a cctaaggag actc 24

<210> 166  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 166  
tggatgagg t gtgcaatggc tggc 24

<210> 167  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 167  
agctctcaga ggctggtcat aggg 24

<210> 168  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 168  
gtcggccctt tcccaggact gaacatgaag agttatgccg gtttcctcac 50

<210> 169  
<211> 2477  
<212> DNA  
<213> Homo sapiens

<400> 169  
cgagggcttt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60  
atttttccct ttcctaacaa gttctaacag ctgttctaac agcttagtcat caggggttct 120  
tcttgcttggaa gaagaaaagg ctgagggcag agcagggcac tctcaactcat ggtgaccagc 180  
tccttgcctc tctgtggata acagagcatg agaaaagtcaa gagatgcagc ggagtggat 240  
gatggaaatgc taaaatatggaa aggaatttttgc tttgtcaatcat cagactctgg gagcagttga 300  
cctggagagc ctgggggagg gcctgcctaa caagcttca aaaaacagga gcgacttcca 360  
ctgggcttggg ataagacgtt cccgttaggtt agggaaagact gggtttagtc ctaatatcaa 420  
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cttaaggggc cagaaataga gatgcttgc taaaataat tttaaaaaaaa gcaagtattt 540  
tatagcataa aggcttagaga cccaaataga taacaggatt ccctgaacat tcctaagagg 600  
gagaaaatgtt gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660  
accaggatgg ggaccctggg tcaggccagc ctcttgctc ctcccgaaa ttatgg 720

tctgaccact ctgccttgc ttttcagaa tcatgtgagg gccaaccggg gaagggtggag 780  
 cagatgagca cacacaggag ccgtctcctc accgcccggc ctctcagcat ggaacagagg 840  
 cagccctggc cccggccct ggaggtggac agccgctctg tggctctgct ctcagtggtc 900  
 tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960  
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 gtaaggaatg caagcgtatt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460  
 acatctgcaaa aagcaaa 2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr  
 1 5 10 15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly  
 20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
 35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
 50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val  
 65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
 85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
 100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val  
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser  
165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn  
450 455 460

Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
465 470 475 480

Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
485 490 495

Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
500 505 510

Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
515 520 525

Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
530 535 540

Leu Tyr Phe Leu Gly Glu Gln Arg  
545 550

<210> 171  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171  
tggaaataccg ctcctgcag 20

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172  
cttctgccct ttggagaaga tggc 24

<210> 173  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 173

ggactcactg gcccaggcct tcaatatcac cagccaggac gat

43

<210> 174

<211> 3106

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1683)..(1683)

<223> a, t, c or g

<400> 174

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gaagtgtgtc caagtccgca tttgagcctt gttctgggc ccagcccaac acctggctt 3060  
ggctcaactgt cctgagttgc agtaaagcta taaccttcaa tcacaa 3106

<210> 175  
<211> 636  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MOD\_RES  
<222> (539)  
<223> Any amino acid

<400> 175

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu  
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Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp  
20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln  
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe  
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp  
65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr  
85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser  
100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly  
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp  
130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
145 150 155 160

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp

165

170

175

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
180 185 190

Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
195 200 205

Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
210 215 220

Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
225 230 235 240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
245 250 255

Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
260 265 270

Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
275 280 285

Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
290 295 300

Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
305 310 315 320

Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
325 330 335

Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
340 345 350

Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
355 360 365

Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
370 375 380

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
385 390 395 400

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
405 410 415

Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val

465	470	475	480
Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn			
485	490	495	
Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp			
500	505	510	
Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser			
515	520	525	
Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr			
530	535	540	
Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr			
545	550	555	560
Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val			
565	570	575	
Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln			
580	585	590	
Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln			
595	600	605	
Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr			
610	615	620	
Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys			
625	630	635	
<210> 176			
<211> 2505			
<212> DNA			
<213> Homo sapiens			
<400> 176			
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ccctggtag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120			
aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgg 180			
ggaatccgac acgtgacggt ctgtccgccc tctcagacta gaggagcgt gtaaacgcca 240			
tggctcccaa gaagctgtcc tgcccttcgtt ccctgtcgct gccgctcagc ctgacgctac 300			
tgctgccccca ggcagacact cggtcgttcg tagtggatag gggtcatgac cggttctcc 360			
tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420			
tgcttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgccc atacagttt 480			
atgtgccctg gaactaccac gagccacagc ctggggtcta taacttaat ggcagccggg 540			
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600			
gacccatcat ctgtgcagag tgggagatgg ggggtctccc atcctgggtt cttcgaaaac 660			
ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctgggtca 720			
aggcttgct gcccaagata tatccatggc tttatcaca tgggggcaac atcattagca 780			
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ctgtgtcagc tgtaacccaa ggactagaga acatgctcaa gttggagcc agtgtgaaca 1140			

tgtacatgtt ccatggaggt accaactttg gatattggaa tggtgccgat aagaaggac 1200  
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 agctatcct caatagact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160  
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 ggtggctcat gcctgtatc ccagcactt gggaggctga gacgggtgga ttacctgagg 2280  
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 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
 1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile  
340 345 350

Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro  
355 360 365

Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu  
370 375 380

Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu  
385 390 395 400

Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr  
405 410 415

Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val  
420 425 430

Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val  
435 440 445

Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr  
450 455 460

Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg  
465 470 475 480

Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro  
485 490 495

Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu  
500 505 510

Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys  
515 520 525

Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr  
530 535 540

Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly  
545 550 555 560

Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr  
565 570 575

Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu  
580 585 590

Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu  
595 600 605

Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu  
610 615 620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
645 650

<210> 178  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 178  
tggctactcc aagaccctgg catg 24

<210> 179  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 179  
tggacaaatc cccttgctca gccc 24

<210> 180  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 180  
gggcttcacc gaagcagtgg acctttatgg tgaccacctg atgtccaggg 50

<210> 181  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 181  
ccagctatga ctatgatgca cc 22

<210> 182  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182  
tggcacccag aatggtgttg gctc 24

<210> 183  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183  
cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184  
<211> 1947  
<212> DNA

<213> Homo sapiens

<400> 184

gcttgaaca cgtctgcaag cccaaagttt agcatctgat tggttatgag gtatttgagt 60  
gcacccacaa tatggcttac atgttggaaaa agcttctcat cagttacata tccattat 120  
gtgttatgg ctttatctgc ctctacactc tcttctgggtt attcaggata cctttgaagg 180  
aatattctt cgaaaaagtc agagaagaga gcagttttag tgacattcca gatgtcaaaa 240  
acgatttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcggt 300  
ttggtgtgtt cttgtcagaa gttagtggaaa ataaaacttag ggaaattagt ttgaaccatg 360  
agtggacatt tgaaaaactc aggacgacaa tttcacgcaa cgcccaggac aacggaggat 420  
tgcatctgtt catgctgtcg ggggtgcccgg atgctgtctt tgacctcaca gacctggatg 480  
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
acccaaga gctccacccctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600  
ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660  
cctgggtgta tttgctcaaa aacccctcgag agttgtactt aataggcaat ttgaactctg 720  
aaaacaataa gatgatagga ctgaaatctc tccgagagtt gcggcacctt aagattctcc 780  
acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840  
caaagtttagt cattcataat gacggcacta aactcttgggactgaacagc cttaaagaaaa 900  
tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020  
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aaattgttac tattccccc tctattaccc atgtcaaaaaa cttggagtca ctttatttct 1140  
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tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattt gtcagaacc 1260  
tgcaacattt gcatatcact gggaaacaaag tggacattct gccaaaacaa ttgtttaat 1320  
gcataaaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaag 1380  
tttgtcagct ctcccagctc actcagctgg agctgaaggg gaactgctt gaccgcctgc 1440  
cagcccgactt gggccagttt cggatgctca agaaaagcgg gcttgggttgaagatcacc 1500  
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agggaaaggaa aaattataat cactaatctt ggttctttt aaattgtttg taacttggat 1860  
gctgccgcta ctgaatgttt acaaatttgc tgcctgctaa agtaaatgat taaattgaca 1920  
tttcttact aaaaaaaaaa aaaaaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile  
1 5 10 15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg  
20 25 30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser  
35 40 45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His  
50 55 60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe  
65 70 75 80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His  
85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln  
100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala  
115 120 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro  
130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu  
145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser  
165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val  
180 185 190

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr  
465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro  
485 490 495

Phe Ala Asn Gly Ile  
500

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 186

cctccctcta ttacccatgt c 21

<210> 187

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 187

gaccaacttt ctctgggagt gagg 24

<210> 188

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 188

gtcactttat ttctctaaca acaagctcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

cccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaactg 60  
actttttta tttctttttt tccatctctg ggccagcttggatcctagg ccgccttggg 120  
aagacatttg tggtttacac acataaggat ctgtgtttgg ggtttcttcttcccttgc 180  
acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
gcacttatct gccttaggtac atcgaagtct tttgacacttcc atacagtgtat tatgcctgtc 300  
atcgctggtg gtatccttggc ggcccttgcctc ctgctgatag ttgtcgtgct ctgtcttac 360  
ttcaaaatac acaacgcgtc aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420  
cacaacccag acaagggtgtg gtgggccaag aacagccagg caaaaaccat tgccacggag 480  
tcttgcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagtt tgattccctg 540  
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agaagaaagg cacagctccc catcagtttca atggaaaata actcagtgcc tgctgggaaac 720  
cagctgctgg agatccctac agagagcttc cactggggc aacccttcca ggaaggagtt 780  
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ctcacacaaa tctaccctt gcgtggctgg aactgacgtt tccctggagg tgcagaaaa 900  
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gagctgacaa tggcggaggg tgaaggcaat gcaagctgca cagtcagttt aggggggtgcc 1080  
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tggacaatag aaagaccaga aaacaaaagc atcagaatattt tctttccta tgcagtttt 1200  
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aacttgcaac taaaagaccc aacttgcaaa cccaaattat caaatgtgtt ggaattttct 1920  
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aatataatca cttttctgc atcctcaact tctgaagtga tcacccgtca gaaacaactc 2040  
cagattattt tgaagtgtga aatggacat aattctacag tggagataat atacataaca 2100  
gaagatgtatg taatacaaag tcaaaatgca ctggccaaat ataacaccag catggcttt 2160  
tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220  
caaactctt ttgttcaagt tagtctgcac acctcagatc caaatttggt ggtgtttctt 2280  
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aaataccaga agctgcagaa ctatataacta acaggtccaa ccctaaatgtt gacatgtttc 2820

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<210> 190  
<211> 607  
<212> PRT  
<213> Homo sapiens

<400> 190  
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Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
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Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
35 40 45  
  
Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
50 55 60  
  
Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
65 70 75 80  
  
Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
85 90 95  
  
Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
100 105 110  
  
Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
115 120 125  
  
Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
130 135 140  
  
Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
145 150 155 160  
  
Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
165 170 175  
  
Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
180 185 190  
  
Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
195 200 205  
  
Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
210 215 220  
  
Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
225 230 235 240  
  
Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val  
565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe  
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr  
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<210> 191

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 191

tctctattcc aaactgtggc g 21

<210> 192

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 192

tttgatgacg attcgaaggt gg 22

<210> 193

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 194

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ctgctgctgc cgccgcccgttcc cacagcgcca cgcgcgttcga ccccacctgg 180  
gagtccctgg acgcccggca gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240  
atccactggg gagtgtttc cgtgcccagc ttcggtagcg agtggttctg gtggatttgg 300  
caaaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagttc 360

aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgccaa ccagtggca 420  
gatattttc aggccctctgg tgccaaatac attgtcttaa cttccaaaca tcataaggc 480  
tttacctgt ggggttcaga atattcgtgg aactgaaatg ccatagatga ggggcccag 540  
aggacattg tcaaggaact tgaggtagcc attagaaca gaactgaccc gcttttgg 600  
ctgtactatt cccttttga atggttcat ccgctcttcc ttgaggatga atccagttca 660  
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aactatcagc ctgagggtct gtggtcggat ggtgacggag gacccggg tcaatactgg 780  
aacagcacag gcttcttggc ctggttataat aatgaaagcc cagttgggg cacagtagtc 840  
accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900  
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taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

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					20										30

Arg	Phe	Asp	Pro	Thr	Trp	Glu	Ser	Leu	Asp	Ala	Arg	Gln	Leu	Pro	Ala
					35										45

Trp	Phe	Asp	Gln	Ala	Lys	Phe	Gly	Ile	Phe	Ile	His	Trp	Gly	Val	Phe
					50										60

Ser	Val	Pro	Ser	Phe	Gly	Ser	Glu	Trp	Phe	Trp	Trp	Tyr	Trp	Gln	Lys
															80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro

	85	90	95
Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe			
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Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr			
115	120	125	
Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser			
130	135	140	
Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp			
145	150	155	160
Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg			
165	170	175	
Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu			
180	185	190	
Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys			
195	200	205	
Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val			
210	215	220	
Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser			
225	230	235	240
Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr			
245	250	255	
Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly			
260	265	270	
Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro			
275	280	285	
His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr			
290	295	300	
Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val			
305	310	315	320
Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn			
325	330	335	
Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg			
340	345	350	
Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr			
355	360	365	
Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val			
370	375	380	
Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu			

385	390	395	400
Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile			
405		410	415
Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn			
420	.	425	430
Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu			
435		440	445
Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr			
450		455	460
Asn Val Ile			
465			
<210> 196			
<211> 23			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic			
oligonucleotide probe			
<400> 196			
tggtttgacc	aggccaagtt	cg	23
<210> 197			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
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<223> Description of Artificial Sequence: Synthetic			
oligonucleotide probe			
<400> 197			
ggattcatcc	tcaaggaaga	gcgg	24
<210> 198			
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<212> DNA			
<213> Artificial Sequence			
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<223> Description of Artificial Sequence: Synthetic			
oligonucleotide probe			
<400> 198			
aacttgcagc	atcagccact	ctgc	24
<210> 199			
<211> 45			
<212> DNA			
<213> Artificial Sequence			

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 199

ttccgtgccc agcttcggta gcgagtggtt ctgggtgtat tggca

45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

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catctgagggt gtttccctgg ctctgaaggg gtaggcacga tggccaggtg cttcagcctg 180  
gtgttgcctc tcacttccat ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240  
gaagagcttt ccatccaggt gtcatgcaga attatgggaa tcacccttgt gagcaaaaag 300  
gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgt gggactaagt 360  
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ggctgggttg gagatggatt cgtggtcata tcttaggatta gcccaaacc caagtgtggg 480  
aaaaatgggg tgggtgtcct gatttggaaag gttccagtga gccgacagtt tgcagcctat 540  
tgttacaact catctgatac ttggactaac tcgtgcattc cagaattat caccaccaa 600  
gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgacagt 660  
acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720  
ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agttttatg 780  
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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
165 170 175

Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
195 200 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
210 215 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Val Pro Thr Ala Leu  
225 230 235 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
245 250 255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
260 265 270

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
275 280 285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
290 295 300

Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
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Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagcttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203

gtcagtgaca gtacctactc gg

22

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204

tggaggcagga ggagtagtag tagg

24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 206  
 <211> 1620  
 <212> DNA  
 <213> Homo sapiens

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 <222> (973)..(973)  
 <223> a, t, c or g

<220>  
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 <222> (977)..(977)  
 <223> a, t, c or g

<220>  
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 <222> (996)..(996)  
 <223> a, t, c or g

<220>  
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 <222> (1003)..(1003)  
 <223> a, t, c or g

<400> 206  
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 accgcagatc catcaactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300  
 ccaacacaat tctttcttc cgcttggata ttcgcattggg cctactttac atcacactct 360  
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 aaggactctt gcttcctt gcccctctgg ctgcgtttat ggtcttcatt aaaagtataa 1380  
 gcctaacttt gtcgttagtc ctaaggagaa accttaacc acaaagttt tatcattgaa 1440  
 gacaatattg aacaacccccc tattttgtgg ggattgagaa ggggtgaata gaggctttag 1500  
 acttccttt gtgtggtagg acttggagga gaaatcccct ggactttcac taaccctctg 1560  
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<210> 207  
<211> 296  
<212> PRT  
<213> Homo sapiens

<400> 207  
Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg  
1 5 10 15  
  
Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu  
20 25 30  
  
Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly  
35 40 45  
  
Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg  
50 55 60  
  
Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn  
65 70 75 80  
  
Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
85 90 95  
  
Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
100 105 110  
  
Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
115 120 125  
  
Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
130 135 140  
  
Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
145 150 155 160  
  
Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
165 170 175  
  
Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
180 185 190  
  
Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
195 200 205  
  
Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
210 215 220  
  
Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
225 230 235 240  
  
Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
245 250 255  
  
Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys  
290 295

<210> 208  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208  
gcttggatat tcgcatgggc ctac 24

<210> 209  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 209  
tggagacaat atccctgagg 20

<210> 210  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 210  
aacagttggc cacagcatgg cagg 24

<210> 211  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 211  
ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
<211> 1985

<212> DNA

<213> Homo sapiens

<400> 212

ggacagctcg cggcccccga gagctctagc cgtcgaggag ctgcctgggg acgtttgcc 60  
tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctccctgg 120  
cccatgtctc ctgctccccg gtcctacgg actgccttc tacaacggct tctactactc 180  
caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240  
gaagctggtg gtggagacac ccgaggagac cctgttcacc tbeccaagggg ccagtgtat 300  
cctgcccctgc cgctaccgct acgagccggc cctggctcc cccggcgtg tgcgtgtcaa 360  
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gaggcaccgc tcctttgggg actaccaagg cccgcgtgcac ctgcggcagg acaaagagca 480  
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agaatgccgc cgggagtcgg ggcatttgcg gtcacagttt ccctggccct cagccctggg 1560  
gaagaagagg gcctcggggg cctccggagc tgggcttgg gcctctcctg cccacacta 1620  
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aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1980  
aaaaaaaaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr  
1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp  
115 120 125

Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr  
130 135 140

Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu  
145 150 155 160

Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg  
165 170 175

Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala  
180 185 190

Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly  
195 200 205

Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr  
210 215 220

Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro  
225 230 235 240

Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp  
245 250 255

Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu  
260 265 270

His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu  
275 280 285

Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys  
290 295 300

Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser  
305 310 315 320

Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu  
325 330 335

Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr  
340 345 350

Gly Val Tyr Cys Tyr Arg Gln His  
355 360

<210> 214  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214  
tgcttcgcta ctgccctc 18

<210> 215  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215  
ttcccttgtg ggttggag 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
agggctggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagtgag gaaatgca 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
 tgtccaaagt acacacacacct gagg 24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaagggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
 ggagagcggga gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60  
 gcttctgttg ctactgaggc acggggccca ggggaagcca tccccagacg caggccctca 120  
 tggccagggg agggtgcacc aggcggccccc cctgagcgcac gctcccccatt atgacgccc 180  
 cgggaacttc cagtagcacc atgaggctt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccg tctggggcgg atcgtggacc gcatggaccg 300  
 cgcggggac ggcgacggct gggtgtcgct ggccgagctt cgcgcgtgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcggtgag cgccggctgg gacacgtacg acacggaccg 420  
 cgacggcgt gtgggttggg aggagctgctgcaacgcccacc tatggccact acgcgcccgg 480  
 tgaagaattt catgacgtgg aggtatgcaga gacctacaaa aagatgtcgatctgg 540  
 gcggcgttccgggtggccg accaggatgg ggactcgatg gcccactcgag aggagctgac 600  
 agccttcctg caccggagg agtccctca catgcgggac atcgtgattt ctgaaaccct 660  
 ggaggacctg gacagaaaaca aagatggcta tgtccaggtg gaggagtaca tcgcggatct 720  
 gtactcagcc gagcctgggg aggaggagcc ggctgggtg cagacggaga ggcagcgtt 780  
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 ccagggaggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260  
 cagccccac ccagggaccc ttggcccaa gctcagctct aagaaccgc ccaaccctc 1320  
 cagctccaaa tctgagcctc caccacatag actgaaactc ccctggccccc agccctctcc 1380  
 tgccctggcct ggcctgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440  
 accttggaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His  
 1 5 10 15

Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly  
20 25 30

Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala  
35 40 45

His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val  
50 55 60

Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu  
65 70 75 80

Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp  
85 90 95

Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg  
100 105 110

His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp  
115 120 125

Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly  
130 135 140

His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr  
145 150 155 160

Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp  
165 170 175

Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu  
180 185 190

His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr  
195 200 205

Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu  
210 215 220

Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala  
225 230 235 240

Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn  
245 250 255

Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro  
260 265 270

Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu  
275 280 285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
325

<210> 222  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 222  
cgcaggccct catggccagg 20

<210> 223  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 223  
gaaatcctgg gtaattgg 18

<210> 224  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 224  
gtgcgcggtg ctcacagctc atc 23

<210> 225  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 225  
cccccctgag cgacgctccc ccatgatgac gcccacggga actt 44

<210> 226  
<211> 2403  
<212> DNA  
<213> Homo sapiens

<400> 226

ggggcccttgc ctccgcact cgggcccgc cgggtggatc tcgagcaggt gcggagcccc 60  
gggcggcggg cgccgggtcg aggatccct gacgcctctg tccctgttc ttgtcgctc 120  
ccagccgtc tgtcgctgtt ttggccccc cgcctcccg cggtgcgggg ttgcacaccc 180  
atccctggct tcgctcgatt tgccggcag ggcctccca gacctagagg ggcgtggcc 240  
tggagcagcg ggtcgctgtt gtcctctctc ctctgcgcg cgcggggga tccgaagggt 300  
gcggggctct gaggaggtga cgcgggggc ctccgcacc ctggcctgc cgcatttctc 360  
cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggctc 420  
tcggccctcggtgtgtctg ctgctgctgc cggggccgc gggcagcag ggagccgctc 480  
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ctcagggaaag aggagataat gtggattaaa accttaagag ttcttaaccat gcctactaaa 2340  
tgtacagata tgcaaattcc atagctcaat aaaagaatct gatacttaga caaaaaaaaa 2400  
aaa 2403

<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu

1

- 5

-10-

15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Ala Pro Ile Ala Ile  
20 25 30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val  
35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn  
50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg  
65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro  
85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln  
100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser  
115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro  
130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys  
145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile  
165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala  
180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln  
195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser  
210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly  
225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
245 250 255

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228  
tggtctcgca caccgatc 18

<210> 229  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 229  
ctgctgtcca caggggag 18

<210> 230  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 230  
ccttgaagca tactgctc 18

<210> 231  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 231  
gagatagcaa tttccgcc 18

<210> 232  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 232  
ttcctcaaga gggcagcc 18

<210> 233  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 233  
cttggcacca atgtccgaga tttc 24

<210> 234  
<211> 45  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 234

gctctgagga aggtgacgca cggggcctcc gaacccttgg ccttg

45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

cgccgcgctc ccgcacccgc ggcccgccca ccgcggcgt cccgcacatcg caccgcagc 60  
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gtcgccggcg cggctgcggg cgcaagcgg agatgcagcg gcttggggcc accctgctgt 180  
gcctgctgtc ggcggccggc gtccccacgg ccccccgcgc cgctccgacg ggcaccccg 240  
ctccagtcggcc gcccggcccg gctctcagct accccgcagga ggaggccacc ctcaatgaga 300  
tgttccgcga ggttggggaa ctgtatggagg acacgcagca caaatgcgc agcgcgggtgg 360  
aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggccaaact 420  
taccccccag ctatcacaat gagaccaaca cagacacgaa gggttggaaat aataccatcc 480  
atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtctttcag 540  
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<210> 236  
<211> 350  
<212> PRT  
<213> Homo sapiens

<400> 236  
Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Ala Ala Ala  
1 5 10 15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
325 330 335

Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
340 345 350

<210> 237

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

ggagctgcac cccttgc

17

<210> 238

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 238

ggaggactgt gccaccatga gagactcttc aaacccaagg caaaaattgg

49

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 239

gcagagcgga gatgcagcgg ctgg

24

<210> 240

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 240  
ttggcagctt catggagg 18

<210> 241  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 241  
cctggcaaaa aatgcaac 18

<210> 242  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 242  
ctccagctcc tggcgcacct cctc 24

<210> 243  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 243  
ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg 45

<210> 244  
<211> 3679  
<212> DNA  
<213> Homo Sapien

<400> 244  
aaggaggctg ggagggaaaga ggtaagaaag gtttagagaac ctacctcaca 50  
tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100  
cactctcctt ccctccaaa cacacatgtg catgtacaca cacacataca 150  
cacacataca cttccctctc cttcactgaa gactcacagt cactcactct 200  
gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcctggcc 250  
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ccaggcacgg tgactcacac ctgtaatccc agcattttgg gagaccgagg 350

tgagcagatc acttgaggtc aggagttcga gaccagcctg gccaacatgg 400  
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gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550  
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aataaaaata aataataaca ataaaaaaaa 3679

<210> 245  
<211> 713  
<212> PRT  
<213> Homo Sapien

<400> 245  
Met Arg Leu Leu Val Ala Pro Leu Leu Leu Ala Trp Val Ala Gly  
1 5 10 15  
Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro  
20 25 30  
Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser  
35 40 45  
Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu  
50 55 60  
Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu  
65 70 75  
Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly  
80 85 90  
Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe  
95 100 105  
Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu  
110 115 120  
Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His  
125 130 135  
Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His  
140 145 150

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser  
155 160 165

Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile  
170 175 180

Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met  
185 190 195

Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg  
200 205 210

Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu  
215 220 225

Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu  
230 235 240

Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg  
245 250 255

Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys  
260 265 270

Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu  
275 280 285

His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser  
290 295 300

Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu  
305 310 315

Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala  
320 325 330

Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn  
335 340 345

Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn  
350 355 360

Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys  
365 370 375

Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile  
380 385 390

Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg  
395 400 405

Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys  
410 415 420

Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val  
425 430 435

Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu  
440 445 450

Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu  
455 460 465

Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly  
470 475 480

Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr  
485 490 495

Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val  
500 505 510

Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu  
515 520 525

Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His  
530 535 540

Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn  
545 550 555

Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr  
560 565 570

Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr  
575 580 585

Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala  
590 595 600

Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr  
605 610 615

Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly  
620 625 630

Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly  
635 640 645

Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly  
650 655 660

Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser  
665 670 675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
680 685 690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
695 700 705

Leu Pro Pro Leu Ser Gln Asn Ser  
710

<210> 246  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 246  
aacaaggtaa gatgccatcc tg 22

<210> 247  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 247  
aaacttgtcg atggagacca gctc 24

<210> 248  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 248  
aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249  
<211> 3401  
<212> DNA  
<213> Homo Sapien

<400> 249  
gcaagccaag gcgctgttg agaaggtgaa gaagttccgg acccatgtgg 50  
aggaggggga cattgtgtac cgcctctaca tgcggcagac catcatcaag 100  
gtgatcaagt tcatcctcat catctgctac accgtctact acgtgcacaa 150  
catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200  
accgcaccta ccgctgtgcc cacccctgg ccacactctt caagatcctg 250  
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cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400  
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gcgcttcgcc gtcttcgtt cgaggatgag tgagaacaag ctgcggcagc 500  
tgaacctcaa caacgagtgg acgctggaca agctccggca gcggctcacc 550  
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ccctgacact gtgttgacc tgggtggagct ggaggtcctc aagctggagc 650  
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aacaagatcg agaagatccc cacccagctc ttctactgcc gcaagctgcg 1350  
ctacctggac ctcagccaca acaacctgac cttccctccct gccgacatcg 1400  
gcctcctgca gaacctccag aacctagcca tcacggccaa ccggatcgag 1450  
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cctctgacaa ccatgaagca aaaatccgtt acatgtgggt ctgaacttgt 3350  
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a 3401

<210> 250

<211> 546  
<212> PRT  
<213> Homo Sapien

<400> 250

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Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
			20						25					30
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
				35					40					45
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
				50					55					60
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
				65					70					75
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
				80					85					90
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys
				95					100					105
Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro
				110					115					120
Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu
				125					130					135
Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp
				140					145					150
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu
				155					160					165
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp
				170					175					180
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val
				185					190					195
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu
				200					205					210
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala
				215					220					225

Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp  
230 235 240

Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu  
245 250 255

Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr  
260 265 270

Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu  
275 280 285

Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp  
290 295 300

Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr  
305 310 315

Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr  
320 325 330

Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser  
335 340 345

Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn  
350 355 360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His  
365 370 375

Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile  
380 385 390

Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
395 400 405

Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
410 415 420

Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
425 430 435

Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
440 445 450

Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
455 460 465

Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
470 475 480

Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
485 490 495

Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly

500	505	510
Glu Cys Pro Leu Leu Lys Arg Ser Gly	Leu Val Val Glu Glu Asp	
515	520	525
Leu Phe Asn Thr Leu Pro Pro Glu Val	Lys Glu Arg Leu Trp Arg	
530	535	540
Ala Asp Lys Glu Gln Ala		
545		

<210> 251  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 251  
caacaatgag ggcaccaagc 20

<210> 252  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 252  
gatggctagg ttctggaggt tctg 24

<210> 253  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 253  
caacctgcag gagattgacc tcaaggacaa caacctaag accatcg 47

<210> 254  
<211> 1650  
<212> DNA  
<213> Homo Sapien

<400> 254  
gcctgttgct gatgctgccc tgcggtaatt gtcattggagc tggcactgcg 50  
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tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
tggattatag tgacggtccg caaggatgcc tacatgttct ggtggctcta 200

ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250  
ggttcaggg cggtccaggc ggttctagca ctggatttg aaactttgag 300  
gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
ccaggctgcc agtctcctat ttgtggataa tccctgggc actgggttca 400  
gttatgtcaa tggtagtggt gcctatgcca aggacctggc tatggtggt 450  
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ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550  
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taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
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gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150  
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tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
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gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550  
ggaggcaatt tggaaattat ttctgcttct taaaaaaaaacc taagatTTT 1600

taaaaaattt atttgtttt atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu  
1 5 10 15

Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp  
20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val  
35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn  
50 55 60

Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln  
65 70 75

Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu  
80 85 90

Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp  
95 100 105

Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr  
110 115 120

Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu  
125 130 135

Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe  
140 145 150

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser  
155 160 165

Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu  
170 175 180

Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly  
185 190 195

Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu  
200 205 210

Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys  
215 220 225

Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala  
230 235 240

Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys

245	250	255
Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr		
260	265	270
Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser		
275	280	285
Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His		
290	295	300
Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly		
305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450
Gln Glu		

<210> 256  
 <211> 1100  
 <212> DNA  
 <213> Homo Sapien

<400> 256  
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 ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150  
 tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctggca 250  
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cgggtggatg gtccagtttgc ccagctgac ttccatgcca tccttctgga 350  
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cctcgctacc tgggaaattc accctatgac attgccttgg tgaagctgtc 450  
tgacacacta acctacacta aacacatcca gcccacatctgt ctccaggcct 500  
ccacatttga gtttggaaac cggacagact gctgggtgac tggctgggg 550  
tacatcaaag aggatgaggc actgccatct ccccacaccc tccaggaagt 600  
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gctgtggtcg gccaatcgcc cccgggtgtct acaccaatat cagccaccac 850  
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<210> 257  
<211> 314  
<212> PRT  
<213> Homo Sapien

<400> 257  
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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser  
20 25 30  
Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly  
35 40 45  
Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg  
50 55 60  
Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg  
65 70 75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
80									85					90
Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser
95									100					105
Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe
110									115					120
Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro
									130					135
Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr
									145					150
Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe
									155					165
Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys
									175					180
Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln
									185					195
Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe	Leu	Lys
									200					210
Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly
									215					225
Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly
									230					240
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val
									245					255
Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val
									260					270
Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met
									275					285
Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu
									290					300
Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val	
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									310					

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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cgagccccga ccagcggagg acgctgcccc caggctgggt gtccctggc 150  
cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
gaatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250  
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aatgattgat acctcaaatg taaaaaa 2427

<210> 259  
<211> 556  
<212> PRT  
<213> Homo Sapien

<400> 259  
Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu  
1 5 10 15  
Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr  
20 25 30  
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu  
35 40 45  
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg  
50 55 60

Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln  
65 70 75

Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg  
80 85 90

Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala  
95 100 105

Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu  
110 115 120

Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly  
125 130 135

Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val  
140 145 150

Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro  
155 160 165

His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser  
170 175 180

Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly  
185 190 195

Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn  
200 205 210

Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln  
215 220 225

Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu  
230 235 240

Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala  
245 250 255

Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly  
260 265 270

Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala  
275 280 285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly  
290 295 300

Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser  
305 310 315

Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp  
320 325 330

Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met  
335 340 345

Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp  
350 355 360

Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg  
365 370 375

Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly  
380 385 390

Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp  
395 400 405

Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser  
410 415 420

Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His  
425 430 435

Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro  
440 445 450

Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg  
455 460 465

Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val  
470 475 480

Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser  
485 490 495

Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln  
500 505 510

His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser  
515 520 525

Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro  
530 535 540

Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu  
545 550 555

Cys

<210> 260  
<211> 1638  
<212> DNA  
<213> Homo Sapien

<400> 260  
gccgcgcgt ctctccggc gccccacacct gtctgagcgg cgcaagcgagc 50  
cgcgccccgg gcgggctgct cggcgccggaa cagtgctcgg catggcaggg 100  
atcccagggc tcctcttcct tctcttctt ctgctctgtg ctgttggca 150  
agtgagccct tacagtgcgg cctggaaacc cacttggcct gcataaccgcc 200

tccctgtcgt cttgccccag tctaccctca atttagccaa gccagactt 250  
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300  
taagggaaact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350  
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcac 400  
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450  
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500  
tcagcattt tgggaaggac ttccctgctca actaccctt ctcacatca 550  
gtgaagttat ccacgggctg caccggcacc ctggtggcag agaagcatgt 600  
cctcacagct gcccactgca tacacgatgg aaaaacctat gtcaaaggaa 650  
cccagaagct tcgagtggc ttccctaaagc ccaagttaa agatggtggt 700  
cgaggggcca acgactccac ttccagccatg cccgagcaga taaaattca 750  
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaaggca 800  
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aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctccctgctaa 900  
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caggcaattt ggttatcgc ttctgtgacg tcaaagacga gacctatgac 1000  
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ttggcattt ttccagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
gatttcaacg tggctgtcag aatcaactcct ctcaaataatg cccagattt 1200  
ctattggatt aaaggaaact acctggattt tagggagggg tgacacagtg 1250  
ttccctcctg gcagcaatta agggcttca tgttcttatt ttaggagagg 1300  
ccaaattgtt tttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgt 1350  
tgtgtgttaag gtgtcttata atctttacc tatttcttac aattgcaaga 1400  
tgactggctt tactatttga aaactggttt gtgtatcata tcataatatca 1450  
tttaaggcagt ttgaaggcat acttttgcatt agaaataaaa aaaatactga 1500  
tttggggcaa tgaggaatat ttgacaattt agttaatctt cacgttttg 1550  
caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600

atatttggca tacaagagat atgaaaaaaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu  
1 5 10 15

Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro  
20 25 30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr  
35 40 45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu  
50 55 60

Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu  
65 70 75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu  
80 85 90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile  
95 100 105

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser  
110 115 120

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser  
125 130 135

Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe  
140 145 150

Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val  
155 160 165

Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly  
170 175 180

Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu  
185 190 195

Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr  
200 205 210

Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys  
215 220 225

Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp  
230 235 240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro  
245 250 255

His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys  
260 265 270

Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp  
275 280 285

Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu  
290 295 300

Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala  
305 310 315

Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln  
320 325 330

Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp  
335 340 345

Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg  
350 355 360

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly  
365 370 375

Asn Tyr Leu Asp Cys Arg Glu Gly  
380

<210> 262  
<211> 1378  
<212> DNA  
<213> Homo Sapien

<400> 262  
gcatcgccct gggctctcg agcctgctgc ctgctccccc gccccaccag 50  
ccatgggtgg ttctggagcg ccccccagccc tgggtgggg ctgtctcggc 100  
acttcacct ccctgctgct gctggcgctcg acagccatcc tcaatgcggc 150  
caggataacct gttcccccag cctgtggaa gccccagcag ctgaaccggg 200  
ttgtggcgcc cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
atccagaaga atgggaccca ccactgcgca gtttctctgc tcaccagccg 300  
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350  
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
cggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450  
ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500  
ccatacagtt ctcagagcgg gtcctgcccc tctgccttacc tgatgcctct 550

atccacacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600  
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
ttccttatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700  
ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750  
ggagcgggat gcttgctgg gcgactccgg gggccccctc atgtgccagg 800  
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850  
gccgagcgcac acaggccccgg ggtctacatc agcctctctg cgacccgctc 900  
ctgggtggag aagatcgtgc aagggtgca gctccgcggg cgcgctcagg 950  
ggggtgtgggc cctcaggca ccgagccagg gctctgggc cgccgcgcgc 1000  
tccttagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
cacatctgga tctggatctg cggcggcctc gggcggttc cccgcggta 1100  
aataggctca tctacctcta cctctgggg cccggacggc tgctgcggaa 1150  
aggaaacccc ctccccgacc cgccccacgg cctcaggccc ccctccaagg 1200  
catcaggccc cgcccaacgg cctcatgtcc cggccccac gacttccggc 1250  
cccgcccccg ggccccagcg ctttgtgta tataaatgtt aatgattttt 1300  
ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263  
<211> 317  
<212> PRT  
<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
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Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
					20					25			30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
					35				40			45		
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
					50			55			60			
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
					65			70			75			

Ala Gly Ser Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His  
80 85 90

Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu  
95 100 105

Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys  
110 115 120

Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys  
125 130 135

Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser  
140 145 150

Ile Gln Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala  
155 160 165

Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp  
170 175 180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu  
185 190 195

Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His  
200 205 210

Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met  
215 220 225

Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly  
230 235 240

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu  
245 250 255

Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn  
260 265 270

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val  
275 280 285

Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly  
290 295 300

Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala  
305 310 315

Arg Ser

<210> 264  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 264  
gtccgcaagg atgcctacat gttc 24

<210> 265  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 265  
gcagaggtgt ctaaggttg 19

<210> 266  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 266  
agctctagac caatgccagc ttcc 24

<210> 267  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 267  
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 268  
gggaaattca ccctatgaca ttgcc 25

<210> 269  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 269

gaatgccctg caagcatcaa ctgg 24

<210> 270  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 270  
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agccggagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
ggcagggat tccagggctc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgatt gctggtagag caag 24

<210> 280

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 280  
ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 281  
cgtctcgagc gctccataca gttcccttgc ccca 34

<210> 282  
<211> 61  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 282  
tggaggggga gcgggatgct tgtctggcg actccgggg ccccctcatg 50  
tgccaggtgg a 61

<210> 283  
<211> 119  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 283  
ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50  
gcagccatct. gtactggcgg ggagcaggac agggacccat cactgaggac 100  
atgctgtgtg ccggctact 119

<210> 284  
<211> 1875  
<212> DNA  
<213> Homo Sapien

<400> 284  
gacggctggc caccatgcac ggctcctgca gtttcctgat gtttctgctg 50

ccgctactgc tactgctggc ggccaccaca ggccccgtt gagccctcac 100  
agatgaggag aaacgtttga tgggtggagct gcacaacctc taccgggccc 150  
aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250  
caaggagcgc gggcgccgag gcgagaatct gttcgccatc acagacgagg 300  
gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
tacaacctca gcgccgccac ctgcagccca ggccagatgt gcggccacta 400  
cacgcagggtg gtatgggcca agacagagag gatcggctgt gttcccact 450  
tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500  
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gtaactgagg ccccatcctt ccggcgact gaagcatcag actctaggaa 700  
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caggccccaa cttccttagc aacgaaagac ccgcctcca tggcaacaga 850  
ggctccaccc tgcgtaacaa ctgaggtccc ttccatccat gcagctcaca 900  
gcctgcctc cttggatgag gagccagttt cttcccaat atcgaccat 950  
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caaggaaact cttacccat gcccaggagg aggctgaggc tgaggctgag 1100  
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ggccctccgg aaggaaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600  
ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650  
ggggtggag gatttggagg agctcaactgc ctacctggcc tggggctgtc 1700  
tgccccacaca gcatgtgcgc tctccctgag tgcctgtta gctggggatg 1750  
gggattccta gggcagatg aaggacaagc cccactggag tggggttctt 1800  
tgagtggggg aggcaaggac gagggaaagga aagtaactcc tgactctcca 1850  
ataaaaacct gtccaaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Leu Leu  
1 5 10 15

Leu Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp  
20 25 30

Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala  
35 40 45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp  
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val  
65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe  
80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu  
95 100 105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys  
110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala  
125 130 135

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu  
140 145 150

Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr  
155 160 165

Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly

	170	175	180
Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser			
185	190	195	
Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro			
200	205	210	
Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser			
215	220	225	
Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile			
230	235	240	
Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys			
245	250	255	
Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr			
260	265	270	
Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr			
275	280	285	
Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu			
290	295	300	
Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile			
305	310	315	
Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser			
320	325	330	
Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly			
335	340	345	
Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu			
350	355	360	
Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro			
365	370	375	
Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr			
380	385	390	
Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser			
395	400	405	
Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser			
410	415	420	
Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser			
425	430	435	
Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly			
440	445	450	
Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe			

455

460

<210> 286  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 286  
tcctgcagtt tcctgatgc 19  
  
<210> 287  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 287  
ctcatattgc acaccagtaa ttcg 24  
  
<210> 288  
<211> 45  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 288  
atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45  
  
<210> 289  
<211> 3662  
<212> DNA  
<213> Homo Sapien  
  
<400> 289  
gttaactgaag tcaggcttt catttggaa gcccccctcaa cagaattcgg 50  
  
tcattctcca agttatggtg gacgtacttc tggatgttc cctctgcttg 100  
cttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaactga 200  
acaacaatga attggagacc attccaaatc tgggaccagt ctcggcaaat 250  
attacacttc tctccttggc tggaaacagg attgttggaa tactccctga 300  
acatctgaaa gagtttcagt cccttggaaac tttggacctt agcagcaaca 350  
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<212> PRT  
<213> Homo Sapien

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Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
35 40 45  
Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
50 55 60  
Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
65 70 75  
Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
80 85 90  
Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
95 100 105  
Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
110 115 120  
Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
125 130 135  
Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
140 145 150  
Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn  
155 160 165

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala  
170 175 180

Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met  
185 190 195

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu  
200 205 210

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly  
215 220 225

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn  
230 235 240

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu  
245 250 255

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser  
260 265 270

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn  
275 280 285

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser  
290 295 300

Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile  
305 310 315

Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg  
320 325 330

Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala  
335 340 345

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn  
350 355 360

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys  
365 370 375

Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys  
380 385 390

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln  
395 400 405

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly  
410 415 420

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp  
425 430 435

Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala  
440 445 450

Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser  
455 460 465

Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu  
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Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln  
485 490 495

Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu  
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Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn  
515 520 525

His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn  
530 535 540

Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg  
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Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro  
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Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro  
575 580 585

Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val  
590 595 600

Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser  
605 610 615

Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
620 625 630

Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp  
635 640 645

Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala  
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Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
665 670 675

Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
680 685 690

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr  
695 700 705

Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val  
710 715 720

Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met

725	730	735
Thr Ala Pro Ser Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly Val	
740	745	750
Val Ile Ile Ala Val Val Cys Cys Val	Val Gly Thr Ser Leu Val	
755	760	765
Trp Val Val Ile Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp Cys	
770	775	780
Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu	Pro Ala Asp Ile Pro	
785	790	795
Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala	Asp Arg Gln Asp Gly	
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Tyr Val Ser Ser Glu Ser Gly Ser His	His Gln Phe Val Thr Ser	
815	820	825
Ser Gly Ala Gly Phe Phe Leu Pro Gln His	Asp Ser Ser Gly Thr	
830	835	840
Cys His Ile Asp Asn Ser Ser Glu Ala Asp	Val Glu Ala Ala Thr	
845	850	855
Asp Leu Phe Leu Cys Pro Phe Leu Gly	Ser Thr Gly Pro Met Tyr	
860	865	870
Leu Lys Gly Asn Val Tyr Gly Ser Asp	Pro Phe Glu Thr Tyr His	
875	880	885
Thr Gly Cys Ser Pro Asp Pro Arg Thr	Val Leu Met Asp His Tyr	
890	895	900
Glu Pro Ser Tyr Ile Lys Lys Glu Cys	Tyr Pro Cys Ser His	
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Pro Ser Glu Glu Ser Cys Glu Arg Ser	Phe Ser Asn Ile Ser Trp	
920	925	930
Pro Ser His Val Arg Lys Leu Leu Asn	Thr Ser Tyr Ser His Asn	
935	940	945
Glu Gly Pro Gly Met Lys Asn Leu Cys	Leu Asn Lys Ser Ser Leu	
950	955	960
Asp Phe Ser Ala Asn Pro Glu Pro Ala	Ser Val Ala Ser Ser Asn	
965	970	975
Ser Phe Met Gly Thr Phe Gly Lys Ala	Leu Arg Arg Pro His Leu	
980	985	990
Asp Ala Tyr Ser Ser Phe Gly Gln Pro	Ser Asp Cys Gln Pro Arg	
995	1000	1005

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
1010 1015 1020

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
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His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
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<211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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gaagctttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200

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<212> PRT  
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Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln  
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Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val  
50 55 60  
Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser  
65 70 75  
Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile  
80 85 90  
Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu  
95 100 105  
Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe  
110 115 120  
Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg  
125 130 135  
Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu  
140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser  
155 160 165  
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly  
170 175 180  
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly  
185 190 195  
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg  
200 205 210  
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp  
215 220 225  
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln  
230 235 240  
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile  
245 250 255  
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val  
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Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp  
275 280 285  
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320 325 330  
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Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
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Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
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Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
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545 550 555

Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
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Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
575 580 585

Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
590 595 600

Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
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Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
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<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn  
215 220 225

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala  
230 235 240

Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met  
245 250 255

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu  
260 265 270

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly  
275 280 285

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn  
290 295 300

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu  
305 310 315

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser  
320 325 330

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn  
335 340 345

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser  
350 355 360

Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile  
365 370 375

Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg  
380 385 390

Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala  
395 400 405

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn  
410 415 420

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys  
425 430 435

Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys  
440 445 450

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln  
455 460 465

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly  
470 475 480

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp  
485 490 495

Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala  
500 505 510

Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser  
515 520 525

Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu  
530 535 540

Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln  
545 550 555

Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu  
560 565 570

Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn  
575 580 585

His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn  
590 595 600

Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg  
605 610 615

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro  
620 625 630

Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro  
635 640 645

Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val  
650 655 660

Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser  
665 670 675

Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
680 685 690

Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp  
695 700 705

Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala  
710 715 720

Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
725 730 735

Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
740 745 750

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr  
755 760 765

Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val  
770 775 780

Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
785 790 795

Thr Ala Pro Ser Leu Asp Asp Gly Trp Ala Thr Val Gly Val  
800 805 810

Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
815 820 825

Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys  
830 835 840

Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
845 850 855

Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
860 865 870

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
875 880 885

Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
890 895 900

Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
905 910 915

Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
920 925 930

Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
935 940 945

Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
950 955 960

Glu Pro Ser Tyr Ile Lys Lys Glu Cys Tyr Pro Cys Ser His  
965 970 975

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
980 985 990

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
995 1000 1005

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
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Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
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Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
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Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
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Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
1070 1075 1080

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
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<210> 297  
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<210> 312  
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<400> 312  
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gggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700  
gggctgacat caagagcgaa tcacaaagat gattaaaggg ttggaaaaaa 1750  
agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800  
agaagactga ggggcaaacc attgatggtt ttcaagtata tgaagggtt 1850  
gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900  
caagaggaaa ctggcttaga cttagtata agggagcatt tcttggcagg 1950  
ggccattgtt agaatacttc ataaaaaaag aagtgtgaaa atctcagtat 2000  
ctctctctct ttctaaaaaa ttagataaaa atttgtctat ttaagatggt 2050  
taaagatgtt cttacccaag gaaaagtaac aaattataga atttcccaa 2100  
agatgtttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150  
taatttggac aaggcttaat ttaggcattt ccctcttgac ctcctaattgg 2200  
agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250  
tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300  
tattccaaat gagagtatga tggacagata ttttagtac tcagtaatgt 2350  
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tcaatttggac tctccaggt tccacagaac agtaatattt tttgaacaat 2650  
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gctgaagatg aaagggaaaa ataaatgaaa atttacttt tcgatgccaa 2850  
tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900  
catcttggttt attatttaat gtttctaaa ataaaaaaatg ttagtggttt 2950  
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aat 3003

<210> 315  
<211> 509  
<212> PRT  
<213> Homo Sapien

<400> 315  
Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu  
1 5 10 15  
  
Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val  
20 25 30  
  
Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys  
35 40 45  
  
Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys  
50 55 60  
  
Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys  
65 70 75  
  
Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu  
80 85 90  
  
Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met  
95 100 105  
  
Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met  
110 115 120  
  
Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met  
125 130 135  
  
Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg  
140 145 150  
  
Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg  
155 160 165  
  
Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys  
170 175 180  
  
Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys  
185 190 195  
  
Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr  
200 205 210  
  
Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys  
215 220 225  
  
Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys  
230 235 240  
  
Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr  
245 250 255

Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro  
260 265 270  
Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn  
275 280 285  
Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro  
290 295 300  
Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr  
305 310 315  
Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro  
320 325 330  
Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr  
335 340 345  
Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala  
350 355 360  
Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln  
365 370 375  
Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val  
380 385 390  
His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu  
395 400 405  
Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly  
410 415 420  
Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys  
425 430 435  
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly  
440 445 450  
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser  
455 460 465  
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala  
470 475 480  
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln  
485 490 495  
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg  
500 505

<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 316  
gatggttcct gctcaagtgc cctg 24

<210> 317  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 317  
ttgcacttgtt aggacccacg tacg 24

<210> 318  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 318  
ctgatggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319  
<211> 2110  
<212> DNA  
<213> Homo Sapien

<400> 319  
ctctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50  
tttagattgt gaaatgtggc tcaaggcttt cacaacttcc ctttcctttg 100  
caacaggtgc ttgctcgaaa ctgaaggtga cagtgccatc acacactgtc 150  
catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200  
cactccagca tcagacatcc agatcatatg gctatttgag agacccca 250  
caatgccccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300  
ttgaaatacc aacacaagtt caccatgatg ccacccaaatg catctctgct 350  
tatcaacccaa ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400  
acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450  
gttgatgatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500  
ggctgtggag tatgtgggaa acatgaccct gacatgccat gtgaaagggg 550

gcactccggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600  
agctccaccc actcctttc tccccaaaac aatacccttc atattgctcc 650  
agtaaccaag gaagacattg ggaattacag ctgcctgggt aggaaccctg 700  
tcagtgaaat gaaaagtgtat atcattatgc ccatcatata ttatggaccc 750  
tatggacttc aagtgaattc tgataaaggg ctaaaagttag gggaaagtgtt 800  
tactgttgac cttggagagg ccatccatt tgattgttct gctgattctc 850  
atccccccaa cacctactcc tggatttagga ggactgacaa tactacat 900  
atcattaagc atgggcctcg cttagaagtt gcatctgaga aagttagccca 950  
gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000  
aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050  
cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100  
atcactat 1150 ttgattat 1150 ccatgtgtct tctcttccta tggaaaaat  
atcaacccta 1200 caaagttata aaacagaaac tagaaggcag gccagaaaca  
gaatacagga 1250 aagctcaa 1250 ac 1250 atttcaggc catgaagatg ctctggatga  
cttcggaata 1300 tatgaattt 1300 gttcttcc agatgttct ggtgttcca  
ggattccaag 1350 caggtctgtt 1350 ccagcctctg attgtgtatc gggcaagat  
ttgcacagta 1400 cagtgtatga agttattcag 1400 cacatccctg cccagcagca  
agaccatcca 1450 gagtgaactt 1450 tcatggct 1450 aacagtacat tcgagtgaaa  
ttctgaagaa 1500 acat 1500 ttaag 1500 gaaaaacagt ggaaaagtat attaatctgg  
aatcagtgaa 1550 gaaaccagga 1550 ccaacac 1550 ctc ttactcatta 1550 ttccttaca  
tgcagaatag 1600 aggcat 1600 tt 1600 gcaaattgaa 1600 ctgcagg 1600 ttcagcatat  
acacaatgtc 1650 ttgtgcaaca 1650 gaaaaacatg 1650 ttggggaaat 1650 attcctcagt  
ggagagtcgt 1700 tctcatgctg 1700 acggggagaa 1700 cggaaagt 1700 gac aggggttcc  
tcataagttt 1750 tgtatgaaat 1750 atctctacaa 1750 acctcaatta 1750 gttctactct  
acactttcac 1800 tatcatcaac 1800 actgagacta 1800 tcctgtctca 1800 cctacaaatg  
tggaaacttt 1850 acattgtcg 1850 attttcagc 1850 agactttgtt 1850 ttattaaatt  
tttatttagt 1900 g 1900 ttaagaatgc 1900 taaattt 1900 at 1900 ttcattttt 1900 atttccaaat  
ttctatctt 1950 g 1950 ttagt 1950 gac 1950 aacaaagtaa 1950 taaggatgg 1950 tgtcacaaaa  
acaaaactat 2000 gc 2000 cttctctt 2000 tttttcaat 2000 caccagtagt 2000 atttttgaga

agacttgtga acacttaagg aaatgactat taaagtctta tttttat 2050  
tttcaaggaa agatggattc aaataaaat 2100  
aaaaaaaaa 2110

<210> 320  
<211> 450  
<212> PRT  
<213> Homo Sapien

<400> 320  
Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly  
1 5 10 15  
Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His  
20 25 30  
Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe  
35 40 45  
His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg  
50 55 60  
Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser  
65 70 75  
Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro  
80 85 90  
Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu  
95 100 105  
Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu  
110 115 120  
Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr  
125 130 135  
Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr  
140 145 150  
Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg  
155 160 165  
Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser  
170 175 180  
Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala  
185 190 195  
Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg  
200 205 210  
Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile  
215 220 225

Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu  
230 235 240

Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu  
245 250 255

Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp  
260 265 270

Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro  
275 280 285

Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp  
290 295 300

Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu  
305 310 315

Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu  
320 325 330

Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly  
335 340 345

Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp  
350 355 360

Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly  
365 370 375

Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His  
380 385 390

Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe  
395 400 405

Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro  
410 415 420

Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr  
425 430 435

Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu  
440 445 450

<210> 321  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 321  
gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccggaggt cttgcagttc ccctggcagt 50

cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aattttatgc cccgtggtgc cctgcttgta aaaaatcttca 200

accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gagcagccag gactgagtg 300

ataactgctc ttcctactat ttatcattgt aaagatgggt aatttaggcg 350

ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400

aagagtggaa gagtattgag cccgtttcat catggttgg tccaggttct 450

gttctgatga gtagtatgtc agcactctt cagctatcta tgtggatcag 500

gacgtgccat aactactta ttgaagacct tggattgcca gtgtgggat 550

catatactgt ttttgctta gcaactctgt tttccggact gttatttagga 600

ctctgtatga tatttggc agattgcctt tgccttcaa aaaggcgcag 650

accacagcca tacccataacc cttcaaaaaa attattatca gaatctgcac 700

aaccttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750  
tcagaagaag aagctgaaag taaagaagga acaaacaaag acttccaca 800  
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
cctagttaaa ttttatagtt atcttaatat tatgatttg ataaaaacag 900  
aagattgatc atttgtttg gttgaagtg aactgtgact ttttgaata 950  
ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000  
acataaaagc actaggata caagttgaa atatgattt agcacagtat 1050  
gatggttaa atagttctt aattttgaa aaatcggtcc aagcaataag 1100  
atttatgtat atttggtaa taataaccta tttcaagtct gagtttgaa 1150  
aatttacatt tcccaagtat tgcattattt aggtatttaa gaagattt 1200  
ttagagaaaa atatttctca tttgatataa ttttctctg tttcactgtg 1250  
tgaaaaaaag aagatatttccataaatgg gaagtttgc cattgtctca 1300  
agaaatgtgt atttcagtga caatttcgtg gtcttttag aggtatattt 1350  
caaaatttcc ttgtatttt aggtatgca actaataaaa actaccttac 1400  
attaatttaat tacagtttc tacacatggt aatacaggat atgctactga 1450  
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atttctctt gtattttct tacttactat gggttacatt ttttattttt 1550  
caaattggat gataatttct tggaaacatt tttttagttt tagtaaacag 1600  
tatttttttgc ttgttcaaa ctgaagtttca ctgagagatc catcaaatttgc 1650  
aacaatctgt tgtaatttaa aattttggcc actttttca gattttacat 1700  
cattcttgct gaactcaac ttgaaattgt ttttttttgc ttttggatg 1750  
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caggaaaaaaag catcttcttgc tataatgttttca aatgtattt ttgtcctcat 1900  
atacagaaaaag ttcttaatttgc attttacagt ctgtaatgct tgatgtttca 1950  
aaataataac attttataat tttttaaaag acaaacttca tattatcctg 2000  
tggcctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050  
gtaggatggaa acattttagt gtattttac tccttaaaga gctagaatac 2100  
atagtttca ccttaaaaaga agggggaaaaa tcataaatac aatgaatcaa 2150

ctgaccatta cgttagtagac aatttctgta atgtccctt ctttcttaggc 2200  
tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250  
ttctttaaag cccttcctt tagaatttaa aatattgtac cattaaagag 2300  
tttggatgtg taacttgtga tgccttagaa aaatatccta agcacaaaaat 2350  
aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaaaa 2397

<210> 325  
<211> 280  
<212> PRT

<213> Homo Sapien

<400> 325  
Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val  
1 5 10 15  
Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn  
20 25 30  
Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly  
35 40 45  
Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln  
50 55 60  
Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp  
65 70 75  
Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
80 85 90  
Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His  
95 100 105  
Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
110 115 120  
Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile  
125 130 135  
Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
140 145 150  
Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys  
155 160 165  
His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
170 175 180  
Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu  
215 220 225

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu  
230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu  
245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser  
260 265 270

Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser  
275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 329  
ttgaaggaca aaggcaatct gccac 25

<210> 330  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 330  
ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45

<210> 331  
<211> 2168  
<212> DNA  
<213> Homo Sapien

<400> 331  
gcgagtgtcc agctgcggag acccgtgata attcgtaac taattcaaca 50  
aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100  
ggacaggcgg attggaagag cgggaaggtc ctggccaga gcagtgtgac 150  
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
ggttggtgt cctgagctgt gtgcaggccg aattttcac ctctattggg 250  
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300  
agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350  
ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400  
tacctggctc accctgtgaa tgcctacaaa ctggtaagc ggctaaacac 450  
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ggaccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650  
caatgctgag tgtggatgac tgctttggga tggccgctc ggcctacaat 700  
gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750  
gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
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ctcaccggcc gcctgcttc cttgaccca agccacgaac gagctggagg 900  
gaatctgcgg tacttgagc agttattgga ggaagagaga gaaaaaacgt 950  
taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000  
aggcctgtgg actacctgcc tgagagggat gttacgaga gcctctgtcg 1050  
tggggaggggt gtcaaactga cacccgtag acagaagagg ctttctgta 1100  
ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaaa 1150  
gaggaggacg agtgggacag cccgcacatc gtcaggtact acgatgtcat 1200  
gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250  
cacgagccac cgttcgtat cccaagacag gagtcctcac tgtcgccagc 1300  
taccgggttt ccaaagctc ctggctagag gaagatgatg accctgttgt 1350  
ggcccgagta aatcgctgga tgcagcatat cacagggta acagtaaaga 1400  
ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450  
ccgcacttcg acttctctag gcgaccttt gacagcggcc tcaaaacaga 1500  
gggaaatagg ttagcgacgt ttcttaacta catgagtgtat gttagaagctg 1550  
gtgggccac cgcttccct gatctgggg ctgcaatttg gcctaagaag 1600  
gttacagctg tttctggta caacctcttgc cgagcgggg aaggtgacta 1650  
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ccaataagtg gttccatgaa cgaggacagg agttcttgag accttggta 1750  
tcaacagaag ttgactgaca tcctttctg tccttccct tcctggcct 1800  
tcagccccatg tcaacgtgac agacacctt gtatgttgc ttgtatgttc 1850  
ctatcaggct gattttgga gaaatgaatg tttgtctgga gcagagggag 1900  
accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950  
gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000  
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gtgtgagatg tttcagtgaa ccaaagttct gataccttgtt ttacatgttt 2100  
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cctaccagaa aaaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
				20					25					30
Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35					40					45
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50					55					60
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65					70					75
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80					85					90
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95					100					105
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110					115					120
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125					130					135
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140					145					150
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155					160					165
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170					175					180
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185					190					195
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Lys	Ser	Gln	Val	Leu	
				200					205					210
Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg
				215					220					225
Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His
				230					235					240
Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu
				245					250					255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu
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Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro  
275 280 285

Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys  
290 295 300

Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His  
305 310 315

Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu  
320 325 330

Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met  
335 340 345

Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys  
350 355 360

Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr  
365 370 375

Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp  
380 385 390

Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile  
395 400 405

Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn  
410 415 420

Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg  
425 430 435

Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala  
440 445 450

Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr  
455 460 465

Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr  
470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
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Pro Cys Gly Ser Thr Glu Val Asp  
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333  
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<210> 334  
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<223> Synthetic Oligonucleotide Probe

<400> 334  
ggacccttct gtgtgccag 19

<210> 335  
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<223> Synthetic Oligonucleotide Probe

<400> 335  
ggtctcaaga actcctgtc 19

<210> 336  
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<223> Synthetic Oligonucleotide Probe

<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337  
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<210> 338  
<211> 2789

<212> DNA  
<213> Homo Sapien

<400> 338

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agacaggaca atcttcttgg ggatgctggt cctggaaagcc agcgggcctt 200  
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cccggtctcc agcagggatg caggtgggtt ctcattggga tgagcggccc 800  
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<210> 339  
<211> 772  
<212> PRT  
<213> Homo Sapien

<400> 339  
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Val Ser Trp Ile Gln Gly Glu Gly Asp Pro Cys Val Glu Ala  
35 40 45  
  
Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg  
50 55 60  
  
Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr  
65 70 75  
  
Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Val Leu Arg Thr Arg  
80 85 90  
  
Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala  
95 100 105  
  
Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val  
110 115 120  
  
Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr  
125 130 135  
  
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser  
140 145 150  
  
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg  
155 160 165  
  
His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile  
170 175 180  
  
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu  
185 190 195  
  
Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala  
200 205 210  
  
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly  
215 220 225  
  
Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg  
230 235 240  
  
Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro  
245 250 255

Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly  
260 265 270

Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu  
275 280 285

Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu  
290 295 300

Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr  
305 310 315

Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr  
320 325 330

Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val  
335 340 345

Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu  
350 355 360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp  
365 370 375

Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala  
380 385 390

Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp  
395 400 405

Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro  
410 415 420

Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg  
425 430 435

Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu  
440 445 450

Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg  
455 460 465

Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met  
470 475 480

Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu  
485 490 495

Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe  
500 505 510

Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu  
515 520 525

Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp  
530 535 540

Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg  
545 550 555

Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala  
560 565 570

Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro  
575 580 585

Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly  
590 595 600

Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp  
605 610 615

Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu  
620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
635 640 645

Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
650 655 660

Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
665 670 675

Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
680 685 690

Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
695 700 705

Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
710 715 720

Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
725 730 735

Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
740 745 750

Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
755 760 765

Gln Glu Gln Ala Asn Ser Thr  
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<211> 1572  
<212> DNA  
<213> Homo Sapien

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cttttgaag ggtgtatgc ttggaagcat tttctgtgct ttgatcacta 150  
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
ttgtaaaacc caaagatgtg agtcttggg ctgcagtaaa ggagacttgg 350  
accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400  
gtttgagtca attaatatgg acacaaatga catgtggta atgatgagaa 450  
aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500  
ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550  
tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600  
aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
cagtttgcct gaaatatgct ggagtattt cagaaaatgc agaagatgct 800  
gatggaaaag atgtatttaa taccaaatct gttggcctt ctattaaaga 850  
ggcaatgact tattttttttt accaggtgtt agaaggctgt tggtttttttt 900  
tggctgttac tttaatggc ctgactccaa atcagatgca tgtgtatgt 950  
tatgggttat accgccttag ggcatttggg catatttca atgatgcatt 1000  
ggttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
agcgtgaata tgatcttgc ataggacgtg tggttcatt attttagt 1100  
gtaactacat atccaataca gctgtatgtt tctttttctt ttctaaattt 1150  
gtggcactgg tataaccaca cattaaagtc agtagtacat tttaaatga 1200  
gggtggtttt ttctttttttt acacatgaac attgtttttttt tttttttttttt 1250  
aagtgtttta agaataataa ttttgcacaaat aaactattaa taaatattat 1300  
atgtgataaa ttctaaattt tgaacattttt aatctgtgg ggcacatattt 1350  
tttgctgttattt ggtttttttttt tttttttttttt tttttttttttt tttttttttttt 1400  
gcaaatgata tctctagttt tgaatttgc atttttttttttt tttttttttttt 1450  
tgtgtgttcc cttaacttctt aatactgttattt tttttttttttt tttttttttttt 1500

gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550

attnaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

<400> 341

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20 25 30

Gly His Gly Asn Arg Met His His His Glu His His His Leu Gln  
35 40 45

Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg  
50 55 60

Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val  
65 70 75

Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp  
80 85 90

Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val  
95 100 105

Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu  
110 115 120

Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp  
125 130 135

Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile  
140 145 150

Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln  
155 160 165

Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr  
170 175 180

Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys  
185 190 195

Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln  
200 205 210

Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val  
215 220 225

Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala  
230 235 240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile  
245 250 255  
Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys  
260 265 270  
Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln  
275 280 285  
Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly  
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Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

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<210> 343

<211> 18

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcg tataaccc 28

<210> 345

<211> 50

<212> DNA

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gggtgtatg cttgaaagca tttctgtgc tttgatcaat atgcttaggac 50

<210> 346  
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<400> 346  
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<400> 347  
ccctcatgtatcc 18

<210> 348  
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<220>  
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<400> 348  
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<210> 349  
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<212> DNA  
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<220>  
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<400> 349  
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<210> 350  
<211> 48  
<212> DNA  
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<220>  
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<210> 351  
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<212> DNA  
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<220>  
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<400> 351  
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<210> 352  
<211> 47  
<212> DNA  
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<220>  
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<400> 352  
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<210> 353  
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<212> DNA  
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<220>  
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<400> 353  
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<210> 354  
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<212> DNA  
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<220>  
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<400> 354  
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<210> 355  
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<212> DNA  
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<220>  
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<400> 355

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<223> Synthetic Oligonucleotide Probe  
  
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<212> DNA  
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<400> 357  
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<400> 358  
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<210> 360  
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<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 360  
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<220>  
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<400> 361  
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<400> 362  
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<210> 363  
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<210> 371  
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<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 373  
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<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

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<211> 48

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 375  
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<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

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agggagggag agaaaaaagag agagagagaa acaaaaaacc aaagagagag 100  
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ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa ttgcacagag 300  
ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350  
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agtggcaatg ggtggacggc acaccttga caaagtctct gagcttctgg 600  
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gagagactct tcaaacccaa ggcaaaatttgaatgtatgtac acctgtttcc 700  
tcaattattt tcggattttgt gaaatggtag gaataaatcc tttgaacaaa 750  
ggaaaatctc tttaagaaca gaaggcacaa ctcaaatgtg taaagaagga 800  
agagcaagaa catggccaca cccaccgccc cacacgagaa atttgcgc 850  
tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 997

<210> 377  
<211> 219  
<212> PRT  
<213> Homo Sapien

<400> 377  
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20 25 30  
Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr  
35 40 45  
Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro

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65	70	75
Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser		
80	85	90
Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu		
95	100	105
Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser		
110	115	120
Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg		
125	130	135
Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp		
140	145	150
Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp		
155	160	165
Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala		
170	175	180
Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val		
185	190	195
Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile		
200	205	210
Asn Pro Leu Asn Lys Gly Lys Ser Leu		
215		

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380  
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<212> DNA  
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<400> 380  
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<210> 381  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 381  
gcagattttg aggacagcca cctcca 26

<210> 382  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 382  
ggccttgca gacaaccgt 18

<210> 383  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 383  
cagactgagg gagatccgag a 21

<210> 384  
<211> 20  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 384  
cagctgccct tccccaaacca 20

<210> 385  
<211> 18

<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 385  
catcaagcgc ctctacca 18

<210> 386  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 386  
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<210> 387  
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<220>  
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<400> 387  
gggccatcac agtccct 18

<210> 388  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 388  
gggatgtggtaa acacacagaa ca 22

<210> 389  
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<212> DNA  
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<400> 389  
tgccagctgc atgctgccag tt 22

<210> 390  
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390  
cagaaggatg tcccggtggaa 20

<210> 391  
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<220>

<223> Synthetic oligonucleotide probe

<400> 391  
gccgcgtgtcc actgcag 17

<210> 392  
<211> 21  
<212> DNA  
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<220>

<223> Synthetic oligonucleotide probe

<400> 392  
gacggcatcc tcagggccac a 21

<210> 393  
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393  
atgtcctcca tgcccacgcg 20

<210> 394  
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<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394  
gagtgcgaca tcgagagctt 20

<210> 395  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 395  
ccgcagcctc agtgatga 18

<210> 396  
<211> 21  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
gaagagcaca gctgcagatc c 21

<210> 397  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
gaggtgtcct ggcttggta gt 22

<210> 398  
<211> 20  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 398  
cctctggcgc ccccactcaa 20

<210> 399  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 399  
ccaggagagc tggcgatg 18

<210> 400  
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<212> DNA  
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<220>  
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<400> 400  
gcaaattcag ggctcaactag aga 23

<210> 401  
<211> 29  
<212> DNA  
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<220>  
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<400> 401  
cacagagcat ttgtccatca gcagttcag 29

<210> 402  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 402  
ggcagagact tccagtcact ga 22

<210> 403  
<211> 22  
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<220>  
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<400> 403  
gccaagggtg gtgttagata gg 22

<210> 404  
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<400> 404  
caggccccct tgatctgtac ccca 24

<210> 405  
<211> 23  
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<220>  
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<400> 405

gggacgtgct tctacaagaa cag 23  
<210> 406  
<211> 26  
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<400> 406  
caggcttaca atgttatgat cagaca 26  
  
<210> 407  
<211> 31  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 407  
tattcagagt tttccattgg cagtgccagt t 31  
  
<210> 408  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 408  
tctacatcag cctctctgcg c 21  
  
<210> 409  
<211> 23  
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<213> Artificial Sequence  
  
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<400> 409  
cgatcttctc cacccaggag cgg 23  
  
<210> 410  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 410  
gccaggcctc acattcgt 18

<210> 411  
<211> 23  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 411  
ctccctgaat ggcagcctga gca 23

<210> 412  
<211> 24

<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 412  
aggtgtttat taagggccta cgct 24

<210> 413  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 413  
cagagcagag ggtgccttg 19

<210> 414  
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<220>  
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<400> 414  
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<210> 415  
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<400> 415  
ccctgtttcc ctatgcata ct 22

<210> 416

<211> 21  
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<223> Synthetic oligonucleotide probe

<400> 416  
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<210> 417  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 417  
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<210> 418  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 418  
gggactgaac tgccagcttc 20

<210> 419  
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<223> Synthetic oligonucleotide probe

<400> 419  
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<400> 420  
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<210> 421  
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<213> Artificial Sequence

<220>

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<400> 421

tctgtccacc atcttgcctt g 21

<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

<400> 422

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atggcgctga ggcggccacc gcgactccgg ctctgcgcctc ggctgcctga 100

cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150

tcaaatccag caatcgaacc ccagtggta c aggaatttga aagtgtggaa 200

ctgtcttgca tcattacgga ttgcagaca agtgacccca ggatcgagtg 250

gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300

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aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400

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ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550

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acccaggaa accagatgga gttaactaca tccgcactga cgaggaggc 950

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<212> PRT  
<213> Homo Sapien

<400> 423  
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Pro Asp Phe Phe Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly  
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Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu

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50	55	60
Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr		
65	70	75
Thr Tyr Val Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly		
80	85	90
Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val		
95	100	105
Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg		
110	115	120
Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val		
125	130	135
Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val		
140	145	150
Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly		
155	160	165
His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu		
170	175	180
Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe		
185	190	195
His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His		
200	205	210
Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala		
215	220	225
Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu		
230	235	240
Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val		
245	250	255
Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly		
260	265	270
Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro		
275	280	285
Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly		
290	295	300
Asp Phe Arg His Lys Ser Ser Phe Val Ile		
305	310	

